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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/346,794	07/02/1999	TERRY P. SNUTCH	NMEDP001-2	2888

25225 7590 03/13/2007

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EXAMINER	
BASI, NIRMAL SINGH	
ART UNIT	**PAPER NUMBER**
1646	

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
3 MONTHS	03/13/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

Office Action Summary	Application No. 09/346,794	Applicant(s) SNUTCH ET AL.	
	Examiner Nirmal S. Basi	Art Unit 1646	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on 05 October 2006.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) 28-31,37 and 40 is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) 28-31,37 and 40 is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)

2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)

3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date 11/21/05

4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.

5) ☐ Notice of Informal Patent Application

6) ☐ Other: _____.

DETAILED ACTION

1. The Board of patent Appeals and Interferences reversed Examiners rejection for lack of utility in the decision dated 11/22/06. The Board further indicated that the effective filing date of the claims appears to be July 2, 1999 since the parent application 09/030482 does not disclose the full-length cDNA, SEQ ID NO:23 (7450 nucleotides long), encoding the rat α_{1G} subunit of a t-type calcium channel. The '482 application provide partial sequences. Therefore, upon further review the priority is not granted to the '482 parent application. The Board decision states, page 10, "Therefore, the claims on appeal do not appear to be supported by the earlier application in the manner required by 35 U.S.C. § 112, first paragraph. Lacking such support, the present claims would not be entitled to the benefit of priority under 35 U.S.C. § 120 based on the earlier-filed application; the effective filing date of the claims appears to be July 2, 1999." Therefore, the present claims are not be entitled to the benefit of priority under 35 U.S.C. § 120 based on the earlier-filed application; the effective filing date of the claims is July 2, 1999.

2. Board of patent Appeals and Interferences decision dated 11/22/06 also states, "On return of this application, however, we recommend that the examiner consider the differences between the method disclosed by Perez-Reyes and the methods defined by the pending claims. If the examiner believes that the differences are such that the claimed methods would have been obvious in view of the prior art method, a rejection

based on 35 U.S.C. § 103 should be entered. If a new rejection is made, of course, Appellants must be given an appropriate opportunity to respond." The examiner has determined the claimed methods are obvious in view of the prior art, a rejection based on 35 U.S.C. § 103 is entered. Appellants are given an appropriate opportunity to respond as required by the Board.

Claim Rejections - 35 USC § 103

3. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

The factual inquiries set forth in *Graham* **v.** *John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was

not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 28-31, 37 and 40 are rejected under 35 U.S.C. 103(a) as being unpatentable over Perez-Reyes (WO 99/29847) or Perez-Reyes (Nature, Vol. 391, pages 900,1998) in view of Harpold et al (US Patent 5,429,921) as it applies to claims 28, 29, 31, 37 and 40, and in view of Brown et al (US Patent 5,688,938) or Okun et al (US Patent 5,8044,36) as it applies to claims 28 and 30 .

The Boards analysis of Perez-Reyes (WO 99/29847) was:

"The amino acid sequences of full-length T-type channels, and the sequences of suitable coding nucleic acids.., at SEQ ID NOs:l-8 (αlG sequences)." Page 6, lines 5-7. Perez-Reyes indicates that SEQ ID NO:5 is derived from rat ("Rattus sp."). See page 37. Amino acids 33 to 2254 of the sequence encoded by Perez-Reyes' SEQ ID NO:5 appear to be virtually identical to amino acids 65 to 2287 of the sequence encoded by the present application's SEQ ID NO:23.

Perez-Reyes discloses a method of identifying a drug which affects T-type calcium channels. The method involves first expressing a T-type calcium channel in a cell to produce an active channel .... The cell expressing the channel is then exposed to a solution containing a putative drug for interfering with the channel. Thereafter, the presence or absence of calcium flux in response to a change in membrane potential is assayed. Page 11, lines 7-12.

Perez-Reyes also includes a working example showing that "mibefradil almost completely abolished T-type current in cells expressing αlG." Page 18. The example is said to "demonstrate[ ] that a cloned T-type calcium channel can be used for identifying a drug which affects T-type calcium channels." Id.. Thus,

Perez-Reyes reasonably appears to disclose a method of identifying drugs that affect T-type calcium channels using cells expressing a rat αlG calcium channel subunit.

However, Perez-Reyes does not reasonably appear to disclose the specific methods defined by claims 28 and 31, the only independent claims remaining in the present application. Claim 28 requires contacting a recombinant cell expressing an αlG subunit "with a known agonist of [a] T-type calcium channel," while claim 31 requires determining binding of a test compound to a cell expressing an αlG subunit "by observing competitive binding with a known agonist or antagonist of [a T-type calcium] channel.

Perez-Reyes does not disclose either of these limitations and therefore does not appear to anticipate the presently pending claims."

The sequence comparisons of the T-type voltage gated calcium channels disclosed by Perez-Reyes (WO 99/29847) are provided as Appendix A, below. Perez-Reyes (WO 99/29847) discloses nucleic acids (AAX83485-AAX83488) encoding T-type voltage gated calcium channel α_{1G} polypeptides. The nucleic acids all have greater than 88% query match and greater than 99% best local similarity with the nucleic acid SEQ ID NO:23 of instant application. Perez-Reyes (WO 99/29847) further discloses polypeptides (AAY14590-AAY14593) comprising T-type voltage gated calcium channel α_{1G} polypeptide. The polypeptides all have greater than 96% query match and greater than 99% best local similarity with the polypeptide of SEQ ID NO:24 of instant application. The nucleic acids (AAX83485-AAX83488) disclosed by Perez-Reyes will

also hybridize under stringent hybridization conditions to the nucleic acid comprising the sequence disclosed in SEQ ID NO:23, absent evidence to the contrary.

Perez-Reyes (Nature, Vol. 391, 1998) discloses a nucleic acid (Accession no. AF027984) which has 99.6% query match and 99.8% best local similarity to SEQ ID NO:23 of instant application (see Appendix B for sequence comparison). Also disclosed is a polypeptide (Accession number T09053) which has 96.9% and 99.7% sequence identity to SEQ ID NO:24 9see Appendix for sequence comparison).

Harpold (US Patent 5,429,921) discloses assays for agonists and antagonists of calcium channels. Harpold discloses (see columns 9-12, claims, specifically claims 1 and 7) methods to identify an agonists or antagonist of a calcium channels which comprise: a) contacting a cell recombinant expressing a heterologous calcium channel with an agonist of said T-type calcium channel; b) contacting said cell with a compound to be tested; and c) determining the ability of said compound for activity as an antagonist (i.e. diminish the activation of subunit by said agonist) or activity as an agonist. The use of controls, which are required to determine functional activity of the calcium channel when testing agonists or antagonists, is disclosed in column 11 (third paragraph).

Column 7 states,

"In an especially preferred embodiment, the invention entails a eukaryotic cell comprising a recombinant calcium channel consisting essentially of human subunits, said recombinant channel being **capable of binding agonist or antagonist** compounds and/or passing calcium channel selective ions. In another of its aspects the invention employs a eukaryotic cell which expresses on its surface functional heterologous calcium channels of the invention in methods for identifying agonists and antagonists of

calcium channel activity in humans and/or assessing the contribution of the various calcium channel subunits to the transport and regulation of calcium ions."

Column 10 discloses that a method of the invention that entails a ligand binding assay for testing a compound for capacity to specifically bind to a calcium channel. Column 16 discloses:

"The capacity of a test compound to bind to membranes comprising heterologous calcium channels or subunits thereof may be determined by any appropriate **competitive binding analysis** (e.g., Scatchard plots), wherein the binding capacity of such membranes is determined in the presence and absence of one or more concentrations of a compound having known affinity for the calcium channel. As a control, these results may be compared to an identically treated membrane preparation from host cells which were not transfected with one or more subunit-encoding nucleic acids (i.e., a negative control).

Okun et al (US Patent 5,804,436) discloses the use of fluorescent dyes in identifying agonists and antagonists of calcium channels. Okun states:

"A development of intracellular fluorescent calcium indicators (Grynkiewicz et all., 1985, is incorporated herein by reference) made it possible for intracellular concentration of free calcium to be measured directly in the living cell. Thus the ability to register changes in intracellular calcium concentration provide the means for monitoring effects of different compounds useful in treating various diseases, whose action is thought to be a result of an interaction with membrane receptors and ion channels."

"A variety of effects caused by the compounds to be screened may be detected and quantitatively characterized according to the present invention. Preferably, these effects include but are not limited to changes in intracellular concentration of ionized calcium, cAMP or pH, transmembrane potential and other physiological and biochemical characteristics of living cell which can be measured by a variety of conventional means, for example using specific fluorescent luminescent or color developing dyes."

"The present invention also includes methods of screening for agonist or antagonist activity of drugs."
"The cells grown in accordance with the preferred embodiments described above, are mixed with an appropriate fluorescent dye for example FURA-2AM for measurements of concentrations of intracellular calcium or BCECF-AM for measurements of intracellular pH, and are incubated in the appropriate conditions to allow the dye to penetrate into the cell. The cells loaded with a dye are supplied to the apparatus. In the apparatus, the cells are successively mixed with a solutions of the compounds to be tested."

Brown (US Patent 5,688,938) discloses the use of fluorescent dyes in identifying agonists and antagonists of calcium channels.

Brown states:

"Changes in Ca^{2+} are readily monitored and quantitated using fluorimetric indicators such as fura-2 or indo-1 (Molecular Probes, Eugene, Oreg.). Measurement of Ca^{2+} provides an assay to assess the ability of molecules to act as agonists or antagonists at the calcium receptor", (see Background of the Invention)."

It would have been prima facie obvious to a person of ordinary skill in the art at the time the invention was made to use the nucleic acid encoding T-type voltage gated calcium channel α_{1G} polypeptides disclosed by Perez-Reyes in the methods for identifying agonists and antagonists for the calcium channels as disclosed by Harpold et al.. The activation could be measured by many techniques well known in the art, for example, using fluorescent dyes as disclosed by Brown and Okun, or measuring the current through the calcium channel as disclosed by Perez-Reyes and Harpold. The ordinary artisan would have been motivated to use the T-type voltage gated calcium channel α_{1G} polypeptides disclosed by Perez-Reyes in the methods of Harpold et al. to identifying agonists and antagonists for the newly discovered T-type voltage gated calcium channel. Perez-Reyes (WO 99/29847) envisions characterizing their newly discovered channel protein, and on page 3 states, "The present invention is useful for exploring the electrophysiological pharmacology of the T-type calcium current. Such knowledge can lead to the development for potentiating or attenuating T-type calcium channels". Page 18 states, when referring to Example 6, "This example demonstrates that a cloned T-Type calcium channel can be used for identifying a drug which affects T-type calcium channels". Newly discovered channel proteins and receptors are routinely assayed for agonists and antagonists using standard methods well accepted in the art. These methods can comprise ligand binding studies or activity studies using well known biochemical techniques and kinetic analysis. The ordinary artisan would have expected success at using the method of Harpold by incorporating the T-type calcium channel of

Perez Reyes to identify agonists and antagonists because many channel proteins have been characterized by their sensitivity to agonists and antagonists (Harpold column 2).

For the reason given above the invention of claims 28-31, 37 and 40 is prima facie obvious.

Applicants can overcome examiners rejection by limiting the methods to identifying antagonists of the T-type calcium channel encoded by the nucleic acid of SEQ ID NO:23 or prescreening compounds as agonists or antagonists of the T-type calcium channel encoded by the nucleic acid of SEQ ID NO:23.

Claim Objections

4. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Upon further review claims 37 and 40 are objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form.

Claim 37 states, when referring to the method of claim 28, "wherein the nucleic acid comprises SEQ ID NO:23." The nucleic acid of claim 28 already comprises SEQ ID NO:23 and claim 37 fails to further limit the nucleic acid.

Claim 40 states, when referring to the method of claim 31, "wherein the nucleic acid comprises SEQ ID NO:23." The nucleic acid of claim 31 already comprises SEQ ID NO:23 and claim 40 fails to further limit the nucleic acid.

5. No claim is allowed.

Advisory

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Nirmal S. Basi whose telephone number is 571-272-0868. The examiner can normally be reached on 9:00 AM-5:30 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Nickol can be reached on 571-272-0835. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

N. S. Basi
Art Unit 1646

NSB Gary B Nickol

GARY B. NICKOL, PH.D.
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

Appendix A

Database search of nucleic acid and polypeptide sequence with the greatest identity to SEQ ID NO :23 and SEQ ID NO:24 are provided below. A comparison of the sequences disclosed by Perez-Reyes, W. (WO 99/29847) that have greatest identity with SEQ ID NO :23 and SEQ ID NO:24 are provided in detail.

```
                         GenCore version 6.2
                 Copyright (c) 1993 - 2007  Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February  9, 2007, 10:25:02 ; Search time 4421 Seconds
                                             (without alignments)
                                             12638.697 Million cell updates/sec

Title:           US-09-346-794-23
Perfect score:   7540
Sequence:        1 ccgtctctggcgcggagcgg..........acgtttgtgcagaatctcta 7540

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters:      11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        N_Geneseq_200701:*
                 1:  geneseqn1980s:*
                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002as:*
                 7:  geneseqn2002bs:*
                 8:  geneseqn2003as:*
                 9:  geneseqn2003bs:*
                 10:  geneseqn2003cs:*
                 11:  geneseqn2003ds:*
```

12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7540	100.0	7540	5	AAF31677	Aaf31677 Rat alpha
2	6956.4	92.3	7286	3	AAZ52309	Aaz52309 Rat pancr
3	6910.4	91.6	6942	13	ADS16295	Ads16295 Rat volta
4	6730.4	89.3	6762	2	AAX83485	Aax83485 Rat T-typ
5	6678.4	88.6	6741	2	AAX83488	Aax83488 Rat T-typ
6	6665	88.4	6795	2	AAX83486	Aax83486 Rat T-typ
7	6661.6	88.4	6816	2	AAX83487	Aax83487 Rat T-typ
8	5810.6	77.1	7741	4	AAD04756	Aad04756 Human T-t
9	5758.4	76.4	7520	14	AEC95681	Aec95681 Calcium c
10	5758.4	76.4	7520	15	AEI99684	Aei99684 Human CCA
11	5497.4	72.9	6750	2	AAX83481	Aax83481 Human T-t
12	5448.2	72.3	8002	4	AAH98402	Aah98402 Human EST
13	5447	72.2	6729	2	AAX83484	Aax83484 Human T-t
14	5432	72.0	6783	2	AAX83482	Aax83482 Human T-t
15	5431.8	72.0	6804	2	AAX83483	Aax83483 Human T-t
16	5431.6	72.0	6807	14	AEE17868	Aee17868 Human cDN
17	5427.2	72.0	6892	5	AAF31684	Aaf31684 Human alp
18	5167.4	68.5	7648	13	ADQ89063	Adq89063 Human uro
19	5167.4	68.5	7648	13	ADS16298	Ads16298 Human vol
20	3891.6	51.6	5337	14	AEC95682	Aec95682 Calcium c
21	3891.6	51.6	5337	15	AEI99685	Aei99685 Human CCA
22	3195	42.4	3993	4	AAS01624	Aas01624 Human T-t
23	3195	42.4	3993	15	AEK52292	Aek52292 Human T-t
24	2363.8	31.4	7277	14	AEC05418	Aec05418 Rat T-typ
25	2363.8	31.4	7426	14	AEC05414	Aec05414 Rat T-typ
26	2363.8	31.4	7432	14	AEC05416	Aec05416 Rat T-typ
27	2351	31.2	7898	2	AAX59080	Aax59080 Human act
28	2351	31.2	7898	8	ABZ58365	Abz58365 Human T-t
29	2349.8	31.2	8447	5	AAF31678	Aaf31678 Rat alpha
30	2348.4	31.1	7898	2	AAX59081	Aax59081 Human act
31	2341.8	31.1	7062	14	AEB12303	Aeb12303 Human T-t
32	2335.8	31.0	7895	14	AEC95664	Aec95664 Calcium c
33	2335.8	31.0	7895	15	AEI99667	Aei99667 Human CCA
34	2291	30.4	6132	2	AAX83489	Aax83489 Human T-t
35	2271	30.1	6114	2	AAX83490	Aax83490 Human T-t
36	1890.8	25.1	6990	13	ADS16296	Ads16296 Human vol
37	1890.8	25.1	6990	14	AEH10223	Aeh10223 Voltage-d
38	1812.2	24.0	2212	5	AAF31681	Aaf31681 Human alp
39	1798	23.8	5562	15	AEF53253	Aef53253 Human CAC
40	1798	23.8	6745	14	ADZ58491	Adz58491 Human alp
41	1796.8	23.8	6816	6	AAS16826	Aas16826 Human T-t
42	1796.8	23.8	6816	8	ABX93560	Abx93560 Human cDN
43	1796.8	23.8	6816	12	ADH69264	Adh69264 Human TCC
44	1796.8	23.8	6855	6	AAS16827	Aas16827 Human T-t
45	1796.8	23.8	6855	8	ABX93561	Abx93561 Human cDN

```
RESULT 4
AAX83485
ID   AAX83485 standard; cDNA; 6762 BP.
XX
AC   AAX83485;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1a) cDNA.
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS   Rattus sp.
XX
PN   WO9929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E,  Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   P-PSDB; AAY14590.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 67-76; 138pp; English.
XX
CC   This sequence represents the coding region for a rat T-type voltage-gated
CC   calcium (Ca) channel alpha-1-G designated rCavT1a. Voltage gated channels
CC   are membrane bound glycosylated proteins formed of several subunits. The
CC   large alpha subunits form a pore in the membrane that is selective for a
CC   given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC   and IV) and each domain contains 6 putative transmembrane helical
CC   segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC   than L- or N-type channels. Characteristics of T-type channels include
CC   short current time, slow activation kinetics near threshold, fast
CC   inactivation kinetics and slow tail current. The sequences AAX83481-
```

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CC   X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC   and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC   comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC   voltage-gated calcium channel proteins can be used to screen for drugs
CC   which affect calcium channels. Methods are also disclosed for treating a
CC   disease or disorder associated with a deficiency in a native T-type
CC   calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 6762 BP; 1362 A; 2044 C; 1917 G; 1439 T; 0 U; 0 Other;

  Query Match             89.3%;  Score 6730.4;  DB 2;  Length 6762;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 6749;  Conservative    0;  Mismatches   11;  Indels    2;  Gaps    1;

Qy        483 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG 60

Qy        543 CAGCTCAACGACCTGTCCGGGGCCGGGGC--GGCAGGGGCCGGGTCGACGGAAAAGGAC 600
              |||||||||||||||||||||||||||||  |   ||| | |||||||||||||||||||
Db         61 CAGCTCAACGACCTGTCCGGGGCCGGGGCCGGCAGGGGCCGGGGTCGACGGAAAAGGAC 120

Qy        601 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 180

Qy        661 TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC 240

Qy        721 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG 300

Qy        781 TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC 360

Qy        841 GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC 420

Qy        901 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTCATTGTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTCATTGTC 480

Qy        961 ATTGCAGGGATGCTGGAGTATTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTGCAGGGATGCTGGAGTATTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG 540

Qy       1021 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCCAGCATGCGCATTCTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCCAGCATGCGCATTCTC 600

Qy       1081 GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC 660

Qy       1141 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      661 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG 720

Qy     1201 TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 780

Qy     1261 ACAGAGAATGAGGACGAGAGCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 ACAGAGAATGAGGACGAGAGCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA 840

Qy     1321 TCCTGCAGGAGTGTGCCCACACTGCGTGGGGAAGGCGGTGGTGGCCCACCCTGCAGTCTG 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 TCCTGCAGGAGTGTGCCCACACTGCGTGGGGAAGGCGGTGGTGGCCCACCCTGCAGTCTG 900

Qy     1381 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT 960

Qy     1441 ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1020

Qy     1501 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG 1080

Qy     1561 TACTTCGTAATGGACGCTCACTCCTTCTACAACTTCATCTACTTCATTCTTCTCATCATC 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 TACTTCGTAATGGACGCTCACTCCTTCTACAACTTCATCTACTTCATTCTTCTCATCATC 1140

Qy     1621 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1200

Qy     1681 ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGTACGATTCCTGTCCAATGCT 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGTACGATTCCTGTCCAATGCT 1260

Qy     1741 AGCACCCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 AGCACCCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1320

Qy     1801 GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCGTG 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCGTG 1380

Qy     1861 CGGGCTGGGCTGCTCAGCAGCCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCCAGTGGC 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 CGGGCTGGGCTGCTCAGCAGCCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCCAGTGGC 1440

Qy     1921 AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC 1500

Qy     1981 CACCATCACCACTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCCAGAG 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 CACCATCACCACTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCCAGAG 1560

Qy     2041 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCCTCTACACCC 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   1561 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCCTCTACACCC 1620

Qy   2101 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 1680

Qy   2161 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCCTCCCAGATGCCCATCGGAGGCATCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCCTCCCAGATGCCCATCGGAGGCATCT 1740

Qy   2221 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAG 1800

Qy   2281 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCTCACC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCTCACC 1860

Qy   2341 AGCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 2400
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Db   1861 AGCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 1920

Qy   2401 ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGA 1980

Qy   2461 GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGTCC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGTCC 2040

Qy   2521 GCTGACCATGTCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GCTGACCATGTCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT 2100

Qy   2581 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGGAGCCTGGGCCCAGAT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGGAGCCTGGGCCCAGAT 2160

Qy   2641 GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC 2220

Qy   2701 GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC 2280

Qy   2761 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2281 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2340

Qy   2821 ATCGTCTTCACCAGCCTCTTCGCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2341 ATCGTCTTCACCAGCCTCTTCGCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC 2400

Qy   2881 TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCATTGTGGTCATCAGTGTG 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2401 TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCATTGTGGTCATCAGTGTG 2460

Qy   2941 TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCTGATG 3000
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        2461 TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCTGATG 2520

Qy        3001 CGGGTGCTGAAGCTGGTGCGCTTCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG 3060
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2521 CGGGTGCTGAAGCTGGTGCGCTTCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG 2580

Qy        3061 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTC 3120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2581 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTC 2640

Qy        3121 AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG 3180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2641 AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG 2700

Qy        3181 TTGCCAGACCGGAAGAATTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT 3240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2701 TTGCCAGACCGGAAGAATTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT 2760

Qy        3241 CTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTTGG 3300
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Db        2761 CTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTTGG 2820

Qy        3301 GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 3360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2821 GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 2880

Qy        3361 GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG 3420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2881 GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG 2940

Qy        3421 CCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG 3480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2941 CCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG 3000

Qy        3481 GTGGCTTTGGGAGAACACGCGGAACTACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT 3540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3001 GTGGCTTTGGGAGAACACGCGGAACTACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT 3060

Qy        3541 ACGGCTGCGACACCAATGTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG 3600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3061 ACGGCTGCGACACCAATGTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG 3120

Qy        3601 GGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT 3660
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Db        3121 GGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT 3180

Qy        3661 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3720
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Db        3181 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3240

Qy        3721 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCCAGCCTAAAGCGG 3780
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Db        3241 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCCAGCCTAAAGCGG 3300

Qy        3781 AGGAGCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        3301 AGGAGCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3360

Qy        3841 GAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACAGG 3900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      3361 GAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACAGG 3420

Qy      3901 GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3421 GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3480

Qy      3961 GGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3481 GGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 3540

Qy      4021 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCCTGAGGACTGATGACCCCCAACTGGATGGG 4080
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Db      3541 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCCTGAGGACTGATGACCCCCAACTGGATGGG 3600

Qy      4081 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTCAGA 4140
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Db      3601 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTCAGA 3660

Qy      4141 TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCCTGGTCGGCCTATATCTTTCCTCCT 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3661 TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCCTGGTCGGCCTATATCTTTCCTCCT 3720

Qy      4201 CAGTCAAGGTTTCGTCTCCTGTGTCACCGGATCATCACCCACAAGATGTTTGACCATGTG 4260
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Db      3721 CAGTCAAGGTTTCGTCTCCTGTGTCACCGGATCATCACCCACAAGATGTTTGACCATGTG 3780

Qy      4261 GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC 4320
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Db      3781 GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC 3840

Qy      4321 CCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACTACATCTTCACGGCAGTCTTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3841 CCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACTACATCTTCACGGCAGTCTTT 3900

Qy      4381 CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3901 CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC 3960

Qy      4441 CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC 4020

Qy      4501 CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG 4080

Qy      4561 CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGGTG 4620
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Db      4081 CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGGTG 4140

Qy      4621 GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC 4200

Qy      4681 TTCTTCATCATTTTTGGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 TTCTTCATCATTTTTGGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT 4260

Qy      4741 CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        4261 CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA 4320

Qy        4801 TGGGTCCGGCACAAGTACAACTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG 4860
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4321 TGGGTCCGGCACAAGTACAACTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG 4380

Qy        4861 CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG 4920
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4381 CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG 4440

Qy        4921 GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC 4980
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4441 GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC 4500

Qy        4981 CTCATCGTGGCCTTCTTTGTCCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCCAT 5040
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4501 CTCATCGTGGCCTTCTTTGTCCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCCAT 4560

Qy        5041 AAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG 5100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4561 AAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG 4620

Qy        5101 AGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCCGAAGCCCAGTGCAAGCCC 5160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4621 AGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCCGAAGCCCAGTGCAAGCCC 4680

Qy        5161 TACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTAC 5220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4681 TACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTAC 4740

Qy        5221 CTGGACCTCTTCATCACTGGTGTCATCGGGCTGAACGTGGTCACTATGGCCATGGAACAT 5280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4741 CTGGACCTCTTCATCACTGGTGTCATCGGGCTGAACGTGGTCACTATGGCCATGGAACAT 4800

Qy        5281 TACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTC 5340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4801 TACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTC 4860

Qy        5341 ATCTTTGTCTTTGAGTCAGTTTTCAAACTTGTGGCCTTTGCGTTCCGCCGTTTCTTCCAG 5400
               ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db        4861 ATCTTTGTCTTTGAGTCAGTTTTCAAACTTGTGGCCTTTGGCTTCCGCCGTTTCTTCCAG 4920

Qy        5401 GACAGGTGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTG 5460
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4921 GACAGGTGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTG 4980

Qy        5461 GAGGAGATTGAGGTCAATCTGTCGCTGCCCATCAACCCCACCATCATCCGTATCATGAGG 5520
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4981 GAGGAGATTGAGGTCAATCTGTCGCTGCCCATCAACCCCACCATCATCCGTATCATGAGG 5040

Qy        5521 GTGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTG 5580
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5041 GTGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTG 5100

Qy        5581 CTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTA 5640
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5101 CTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTA 5160

Qy        5641 TTGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAG 5700
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        5161 TTGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAG 5220

Qy        5701 ACACACCCTTGTGAGGGCTTGGGTCGGCATGCCACCTTTAGGAACTTTGGTATGGCCTTT 5760
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5221 ACACACCCTTGTGAGGGCTTGGGTCGGCATGCCACCTTTAGGAACTTTGGTATGGCCTTT 5280

Qy        5761 CTGACCCTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACCCTTCC 5820
               |||||||||||||||||||||||||||||||||||||||||||||||||||||| |   |
Db        5281 CTGACCCTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACACCCTC 5340

Qy        5821 CGGGACTGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTGTG 5880
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5341 CGGGACTGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTGTG 5400

Qy        5881 TCCTTCGTGCTGACGGCCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAG 5940
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5401 TCCTTCGTGCTGACGGCCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAG 5460

Qy        5941 CACCTGGAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAG 6000
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5461 CACCTGGAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAG 5520

Qy        6001 CTGGAGATGAAGACGCTCAGCCCGCAGCCCCACTCCCCGCTGGGCAGCCCCTTCCTCTGG 6060
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5521 CTGGAGATGAAGACGCTCAGCCCGCAGCCCCACTCCCCGCTGGGCAGCCCCTTCCTCTGG 5580

Qy        6061 CCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACT 6120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5581 CCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACT 5640

Qy        6121 GCCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCCACGATGGTACCCCACCCC 6180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5641 GCCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCCACGATGGTACCCCACCCC 5700

Qy        6181 GAGGAGGTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTCAGC 6240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5701 GAGGAGGTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTCAGC 5760

Qy        6241 CGGACGCACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGA 6300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5761 CGGACGCACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGA 5820

Qy        6301 TCCCTAGGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCGTT 6360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5821 TCCCTAGGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCGTT 5880

Qy        6361 CACTCCCAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATCTG 6420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5881 CACTCCCAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATCTG 5940

Qy        6421 CTCCAGCCTCATGGGGCTCCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCCGC 6480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5941 CTCCAGCCTCATGGGGCTCCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCCGC 6000

Qy        6481 TCCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGAT 6540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6001 TCCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGAT 6060

Qy        6541 GTGCAGGGCCTGGGTAGCCGGGAAGACCTGTTGTCAGAGGTGAGTGGGCCCTCCTGCCCT 6600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db   6061 GTGCAGGGCCTGGGTAGCCGGGAAGACCTGTTGTCAGAGGTGAGTGGGCCCTCCTGCCCT 6120

Qy   6601 CTGACCCGGTCCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGC 6660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6121 CTGACCCGGTCCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGC 6180

Qy   6661 ATCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCTTGCCCAGGCCTGGAACCC 6720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6181 ATCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCTTGCCCAGGCCTGGAACCC 6240

Qy   6721 AGCTGGGCCAAGGACCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGC 6780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6241 AGCTGGGCCAAGGACCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGC 6300

Qy   6781 TGGATTTCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCCTGTTCCCACGGGACCTG 6840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6301 TGGATTTCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCCTGTTCCCACGGGACCTG 6360

Qy   6841 AAGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGAT 6900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6361 AAGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGAT 6420

Qy   6901 GAACAGCGGAGACACTCCATTGCTGTCAGCTGTCTGGACAGCGGCTCCCAACCCCGCCTA 6960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6421 GAACAGCGGAGACACTCCATTGCTGTCAGCTGTCTGGACAGCGGCTCCCAACCCCGCCTA 6480

Qy   6961 TGTCCAAGCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCCTGGGAGCCGGCCTAAG 7020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6481 TGTCCAAGCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCCTGGGAGCCGGCCTAAG 6540

Qy   7021 AAAAAACTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCC 7080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6541 AAAAAACTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCC 6600

Qy   7081 CCATGCAGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATCCC 7140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6601 CCATGCAGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATCCC 6660

Qy   7141 TCGGTCTCCAGCCCCCTTGACAGCACGGCTGCCTCACCCTCCCCAAAGAAAGACACGCTG 7200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6661 TCGGTCTCCAGCCCCCTTGACAGCACGGCTGCCTCACCCTCCCCAAAGAAAGACACGCTG 6720

Qy   7201 AGTCTCTCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC 7242
          ||||||||||||||||||||||||||||||||||||||||||
Db   6721 AGTCTCTCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC 6762
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RESULT 5
AAX83488
ID   AAX83488 standard; cDNA; 6741 BP.
XX
AC   AAX83488;
XX
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DT   07-DEC-1999  (first entry)
XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1d) cDNA.
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS   Rattus sp.
XX
PN   WO9929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E,  Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   P-PSDB; AAY14593.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 94-103; 138pp; English.
XX
CC   This sequence represents the coding region for a rat T-type voltage-gated
CC   calcium (Ca) channel alpha-1-G designated rCavT1d. Voltage gated channels
CC   are membrane bound glycosylated proteins formed of several subunits. The
CC   large alpha subunits form a pore in the membrane that is selective for a
CC   given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC   and IV) and each domain contains 6 putative transmembrane helical
CC   segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC   than L- or N-type channels. Characteristics of T-type channels include
CC   short current time, slow activation kinetics near threshold, fast
CC   inactivation kinetics and slow tail current. The sequences AAX83481-
CC   X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC   and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC   comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC   voltage-gated calcium channel proteins can be used to screen for drugs
CC   which affect calcium channels. Methods are also disclosed for treating a
CC   disease or disorder associated with a deficiency in a native T-type
CC   calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 6741 BP; 1355 A; 2041 C; 1908 G; 1437 T; 0 U; 0 Other;

  Query Match             88.6%;  Score 6678.4;  DB 2;  Length 6741;
  Best Local Similarity   99.5%;  Pred. No. 0;
  Matches 6728;  Conservative    0;  Mismatches   11;  Indels   23;  Gaps    2;

Qy        483 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG 60

Qy        543 CAGCTCAACGACCTGTCCGGGGCCGGGGGC--GGCAGGGGCCGGGTCGACGGAAAAGGAC 600
              ||||||||||||||||||||||||||||||  |   ||| ||||||||||||||||||||
Db         61 CAGCTCAACGACCTGTCCGGGGCCGGGGGCCGGCAGGGGCCGGGGTCGACGGAAAAGGAC 120
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Qy        601 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 180

Qy        661 TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC 240

Qy        721 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG 300

Qy        781 TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC 360

Qy        841 GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC 420

Qy        901 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTCATTGTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTCATTGTC 480

Qy        961 ATTGCAGGGATGCTGGAGTATTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTGCAGGGATGCTGGAGTATTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG 540

Qy       1021 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCCAGCATGCGCATTCTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCCAGCATGCGCATTCTC 600

Qy       1081 GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC 660

Qy       1141 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG 720

Qy       1201 TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 780

Qy       1261 ACAGAGAATGAGGACGAGAGCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACAGAGAATGAGGACGAGAGCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA 840

Qy       1321 TCCTGCAGGAGTGTGCCCACACTGCGTGGGGAAGGCGGTGGTGGCCCACCCTGCAGTCTG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCCTGCAGGAGTGTGCCCACACTGCGTGGGGAAGGCGGTGGTGGCCCACCCTGCAGTCTG 900

Qy       1381 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT 960

Qy       1441 ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1020
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Qy        1501 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG 1080

Qy        1561 TACTTCGTAATGGACGCTCACTCCTTCTACAACTTCATCTACTTCATTCTTCTCATCATC 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 TACTTCGTAATGGACGCTCACTCCTTCTACAACTTCATCTACTTCATTCTTCTCATCATC 1140

Qy        1621 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1200

Qy        1681 ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGTACGATTCCTGTCCAATGCT 1740
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGTACGATTCCTGTCCAATGCT 1260

Qy        1741 AGCACCCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1800
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 AGCACCCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1320

Qy        1801 GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCGTG 1860
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCGTG 1380

Qy        1861 CGGGCTGGGCTGCTCAGCAGCCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCCAGTGGC 1920
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CGGGCTGGGCTGCTCAGCAGCCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCCAGTGGC 1440

Qy        1921 AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC 1980
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC 1500

Qy        1981 CACCATCACCACTACCACCTGGGTAATGGACGCTCAGAGTTCCCCGGGCCAGCCCAGAG 2040
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 CACCATCACCACTACCACCTGGGTAATGGACGCTCAGAGTTCCCCGGGCCAGCCCAGAG 1560

Qy        2041 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCCTCTACACCC 2100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCCTCTACACCC 1620

Qy        2101 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 2160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 1680

Qy        2161 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCCTCCCAGATGCCCATCGGAGGCATCT 2220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1681 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCCTCCCAGATGCCCATCGGAGGCATCT 1740

Qy        2221 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAG 2280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1741 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAG 1800

Qy        2281 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCTCACC 2340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1801 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCTCACC 1860

Qy        2341 AGCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 2400
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1861 AGCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 1920
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Qy    2401 ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGA 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1921 ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGA 1980

Qy    2461 GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGTCC 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1981 GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGTCC 2040

Qy    2521 GCTGACCATGTCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2041 GCTGACCATGTCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT 2100

Qy    2581 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGGAGCCTGGGCCCAGAT 2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2101 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGGAGCCTGGGCCCAGAT 2160

Qy    2641 GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC 2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2161 GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC 2220

Qy    2701 GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC 2760
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2221 GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC 2280

Qy    2761 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2281 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2340

Qy    2821 ATCGTCTTCACCAGCCTCTTCGCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC 2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2341 ATCGTCTTCACCAGCCTCTTCGCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC 2400

Qy    2881 TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCATTGTGGTCATCAGTGTG 2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2401 TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCATTGTGGTCATCAGTGTG 2460

Qy    2941 TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCTGATG 3000
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2461 TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCTGATG 2520

Qy    3001 CGGGTGCTGAAGCTGGTGCGCTTCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG 3060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2521 CGGGTGCTGAAGCTGGTGCGCTTCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG 2580

Qy    3061 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTC 3120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2581 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTC 2640

Qy    3121 AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG 3180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2641 AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG 2700

Qy    3181 TTGCCAGACCGGAAGAATTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT 3240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2701 TTGCCAGACCGGAAGAATTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT 2760

Qy    3241 CTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTTGG 3300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2761 CTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTTGG 2820
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Qy   3301 GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 2880

Qy   3361 GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG 2940

Qy   3421 CCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG 3000

Qy   3481 GTGGCTTTGGGAGAACACGCGGAACTACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GTGGCTTTGGGAGAACACGCGGAACTACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT 3060

Qy   3541 ACGGCTGCGACACCAATGTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 ACGGCTGCGACACCAATGTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG 3120

Qy   3601 GGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT 3180

Qy   3661 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3240

Qy   3721 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCCAGCCTAAAGCGG 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCCAGCCTAAAGCGG 3300

Qy   3781 AGGAGCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 AGGAGCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3360

Qy   3841 GAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACAGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACAGG 3420

Qy   3901 GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3480

Qy   3961 GGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 3540

Qy   4021 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCCTGAGGACTGATGACCCCCAACTGGATGGG 4080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCCTGAGGACTGATGACCCCCAACTGGATGGG 3600

Qy   4081 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTCAGA 4140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTCAGA 3660

Qy   4141 TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCCTGGTCGGCCTATATCTTTCCTCCT 4200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCCTGGTCGGCCTATATCTTTCCTCCT 3720
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Qy       4201 CAGTCAAGGTTTCGTCTCCTGTGTCACCGGATCATCACCCACAAGATGTTTGACCATGTG 4260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3721 CAGTCAAGGTTTCGTCTCCTGTGTCACCGGATCATCACCCACAAGATGTTTGACCATGTG 3780

Qy       4261 GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC 4320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3781 GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC 3840

Qy       4321 CCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACTACATCTTCACGGCAGTCTTT 4380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3841 CCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACTACATCTTCACGGCAGTCTTT 3900

Qy       4381 CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC 4440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3901 CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC 3960

Qy       4441 CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC 4500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3961 CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC 4020

Qy       4501 CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG 4560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4021 CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG 4080

Qy       4561 CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGGTG 4620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4081 CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGGTG 4140

Qy       4621 GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC 4680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4141 GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC 4200

Qy       4681 TTCTTCATCATTTTTGGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT 4740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4201 TTCTTCATCATTTTTGGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT 4260

Qy       4741 CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA 4800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4261 CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA 4320

Qy       4801 TGGGTCCGGCACAAGTACAACTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG 4860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4321 TGGGTCCGGCACAAGTACAACTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG 4380

Qy       4861 CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG 4920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4381 CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG 4440

Qy       4921 GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC 4980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4441 GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC 4500

Qy       4981 CTCATCGTGGCCTTCTTTGTCCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCCAT 5040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4501 CTCATCGTGGCCTTCTTTGTCCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCCAT 4560

Qy       5041 AAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG 5100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4561 AAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG 4620
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Qy     5101 AGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCCGAAGCCCAGTGCAAGCCC 5160
            ||||||||||||||||||||||                     |||||||||||||||||
Db     4621 AGGCTGGAGAAAAAGAGAAGGA---------------------AAGCCCAGTGCAAGCCC 4659

Qy     5161 TACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTAC 5220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4660 TACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTAC 4719

Qy     5221 CTGGACCTCTTCATCACTGGTGTCATCGGGCTGAACGTGGTCACTATGGCCATGGAACAT 5280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4720 CTGGACCTCTTCATCACTGGTGTCATCGGGCTGAACGTGGTCACTATGGCCATGGAACAT 4779

Qy     5281 TACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTC 5340
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4780 TACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTC 4839

Qy     5341 ATCTTTGTCTTTGAGTCAGTTTTCAAACTTGTGGCCTTTGCGTTCCGCCGTTTCTTCCAG 5400
            ||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Db     4840 ATCTTTGTCTTTGAGTCAGTTTTCAAACTTGTGGCCTTTGGCTTCCGCCGTTTCTTCCAG 4899

Qy     5401 GACAGGTGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTG 5460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4900 GACAGGTGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTG 4959

Qy     5461 GAGGAGATTGAGGTCAATCTGTCGCTGCCCATCAACCCCACCATCATCCGTATCATGAGG 5520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4960 GAGGAGATTGAGGTCAATCTGTCGCTGCCCATCAACCCCACCATCATCCGTATCATGAGG 5019

Qy     5521 GTGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTG 5580
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5020 GTGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTG 5079

Qy     5581 CTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTA 5640
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5080 CTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTA 5139

Qy     5641 TTGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAG 5700
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5140 TTGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAG 5199

Qy     5701 ACACACCCTTGTGAGGGCTTGGGTCGGCATGCCACCTTTAGGAACTTTGGTATGGCCTTT 5760
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5200 ACACACCCTTGTGAGGGCTTGGGTCGGCATGCCACCTTTAGGAACTTTGGTATGGCCTTT 5259

Qy     5761 CTGACCCTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACCCTTCC 5820
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |   |
Db     5260 CTGACCCTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACACCCTC 5319

Qy     5821 CGGGACTGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTGTG 5880
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5320 CGGGACTGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTGTG 5379

Qy     5881 TCCTTCGTGCTGACGGCCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAG 5940
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5380 TCCTTCGTGCTGACGGCCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAG 5439

Qy     5941 CACCTGGAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAG 6000
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5440 CACCTGGAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAG 5499
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Qy    6001 CTGGAGATGAAGACGCTCAGCCCGCAGCCCCACTCCCCGCTGGGCAGCCCCTTCCTCTGG 6060
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5500 CTGGAGATGAAGACGCTCAGCCCGCAGCCCCACTCCCCGCTGGGCAGCCCCTTCCTCTGG 5559

Qy    6061 CCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACT 6120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5560 CCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACT 5619

Qy    6121 GCCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCCACGATGGTACCCCACCCC 6180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5620 GCCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCCACGATGGTACCCCACCCC 5679

Qy    6181 GAGGAGGTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTCAGC 6240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5680 GAGGAGGTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTCAGC 5739

Qy    6241 CGGACGCACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGA 6300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5740 CGGACGCACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGA 5799

Qy    6301 TCCCTAGGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCGTT 6360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5800 TCCCTAGGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCGTT 5859

Qy    6361 CACTCCCAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATCTG 6420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5860 CACTCCCAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATCTG 5919

Qy    6421 CTCCAGCCTCATGGGGCTCCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCCGC 6480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5920 CTCCAGCCTCATGGGGCTCCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCCGC 5979

Qy    6481 TCCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGAT 6540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    5980 TCCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGAT 6039

Qy    6541 GTGCAGGGCCTGGGTAGCCGGGAAGACCTGTTGTCAGAGGTGAGTGGGCCCTCCTGCCCT 6600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6040 GTGCAGGGCCTGGGTAGCCGGGAAGACCTGTTGTCAGAGGTGAGTGGGCCCTCCTGCCCT 6099

Qy    6601 CTGACCCGGTCCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGC 6660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6100 CTGACCCGGTCCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGC 6159

Qy    6661 ATCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCTTGCCCAGGCCTGGAACCC 6720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6160 ATCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCTTGCCCAGGCCTGGAACCC 6219

Qy    6721 AGCTGGGCCAAGGACCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGC 6780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6220 AGCTGGGCCAAGGACCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGC 6279

Qy    6781 TGGATTTCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCCTGTTCCCACGGGACCTG 6840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6280 TGGATTTCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCCTGTTCCCACGGGACCTG 6339

Qy    6841 AAGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGAT 6900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    6340 AAGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGAT 6399
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Qy        6901 GAACAGCGGAGACACTCCATTGCTGTCAGCTGTCTGGACAGCGGCTCCCAACCCCGCCTA 6960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6400 GAACAGCGGAGACACTCCATTGCTGTCAGCTGTCTGGACAGCGGCTCCCAACCCCGCCTA 6459

Qy        6961 TGTCCAAGCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCCTGGGAGCCGGCCTAAG 7020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6460 TGTCCAAGCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCCTGGGAGCCGGCCTAAG 6519

Qy        7021 AAAAAACTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCC 7080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6520 AAAAAACTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCC 6579

Qy        7081 CCATGCAGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATCCC 7140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6580 CCATGCAGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATCCC 6639

Qy        7141 TCGGTCTCCAGCCCCCTTGACAGCACGGCTGCCTCACCCTCCCCAAAGAAAGACACGCTG 7200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        6640 TCGGTCTCCAGCCCCCTTGACAGCACGGCTGCCTCACCCTCCCCAAAGAAAGACACGCTG 6699

Qy        7201 AGTCTCTCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC 7242
               ||||||||||||||||||||||||||||||||||||||||||
Db        6700 AGTCTCTCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC 6741
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RESULT 6
AAX83486
ID   AAX83486 standard; cDNA; 6795 BP.
XX
AC   AAX83486;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1b) cDNA.
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS   Rattus sp.
XX
PN   WO9929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E, Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   P-PSDB; AAY14591.
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XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 76-85; 138pp; English.
XX
CC   This sequence represents the coding region for a rat T-type voltage-gated
CC   calcium (Ca) channel alpha-1-G designated rCavT1b. Voltage gated channels
CC   are membrane bound glycosylated proteins formed of several subunits. The
CC   large alpha subunits form a pore in the membrane that is selective for a
CC   given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC   and IV) and each domain contains 6 putative transmembrane helical
CC   segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC   than L- or N-type channels. Characteristics of T-type channels include
CC   short current time, slow activation kinetics near threshold, fast
CC   inactivation kinetics and slow tail current. The sequences AAX83481-
CC   X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC   and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC   comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC   voltage-gated calcium channel proteins can be used to screen for drugs
CC   which affect calcium channels. Methods are also disclosed for treating a
CC   disease or disorder associated with a deficiency in a native T-type
CC   calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 6795 BP; 1366 A; 2055 C; 1923 G; 1451 T; 0 U; 0 Other;

  Query Match             88.4%;  Score 6665;  DB 2;  Length 6795;
  Best Local Similarity   99.1%;  Pred. No. 0;
  Matches 6735;  Conservative    0;  Mismatches   25;  Indels   35;  Gaps    2;

Qy        483 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG 60

Qy        543 CAGCTCAACGACCTGTCCGGGGCCGGGGGC--GGCAGGGGCCGGGTCGACGGAAAAGGAC 600
              ||||||||||||||||||||||||||||||  |   ||| | ||||||||||||||||||
Db         61 CAGCTCAACGACCTGTCCGGGGCCGGGGGCCGGCAGGGGCCGGGGTCGACGGAAAAGGAC 120

Qy        601 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 180

Qy        661 TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC 240

Qy        721 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG 300

Qy        781 TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC 360

Qy        841 GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC 420

Qy        901 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTCATTGTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTCATTGTC 480
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Qy    961 ATTGCAGGGATGCTGGAGTATTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ATTGCAGGGATGCTGGAGTATTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG 540

Qy   1021 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCCAGCATGCGCATTCTC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCCAGCATGCGCATTCTC 600

Qy   1081 GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC 660

Qy   1141 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG 720

Qy   1201 TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 780

Qy   1261 ACAGAGAATGAGGACGAGAGCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ACAGAGAATGAGGACGAGAGCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA 840

Qy   1321 TCCTGCAGGAGTGTGCCCACACTGCGTGGGGAAGGCGGTGGTGGCCCACCCTGCAGTCTG 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TCCTGCAGGAGTGTGCCCACACTGCGTGGGGAAGGCGGTGGTGGCCCACCCTGCAGTCTG 900

Qy   1381 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT 960

Qy   1441 ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1020

Qy   1501 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG 1080

Qy   1561 TACTTCGTAATGGACGCTCACTCCTTCTACAACTTCATCTACTTCATTCTTCTCATCATC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 TACTTCGTAATGGACGCTCACTCCTTCTACAACTTCATCTACTTCATTCTTCTCATCATC 1140

Qy   1621 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1200

Qy   1681 ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGTACGATTCCTGTCCAATGCT 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGTACGATTCCTGTCCAATGCT 1260

Qy   1741 AGCACCCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 AGCACCCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1320

Qy   1801 GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCGTG 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCGTG 1380
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Qy   1861 CGGGCTGGGCTGCTCAGCAGCCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCCAGTGGC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CGGGCTGGGCTGCTCAGCAGCCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCCAGTGGC 1440

Qy   1921 AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC 1500

Qy   1981 CACCATCACCACTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCCAGAG 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 CACCATCACCACTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCCAGAG 1560

Qy   2041 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCCTCTACACCC 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCCTCTACACCC 1620

Qy   2101 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1621 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 1680

Qy   2161 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCCTCCCAGATGCCCATCGGAGGCATCT 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1681 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCCTCCCAGATGCCCATCGGAGGCATCT 1740

Qy   2221 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAG 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1741 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAG 1800

Qy   2281 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCTCACC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1801 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCTCACC 1860

Qy   2341 AGCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1861 AGCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 1920

Qy   2401 ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGA 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1921 ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGA 1980

Qy   2461 GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGTCC 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1981 GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGTCC 2040

Qy   2521 GCTGACCATGTCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2041 GCTGACCATGTCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT 2100

Qy   2581 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGGAGCCTGGGCCCAGAT 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2101 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGGAGCCTGGGCCCAGAT 2160

Qy   2641 GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2161 GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC 2220

Qy   2701 GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC 2760
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2221 GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC 2280
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Qy      2761 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2340

Qy      2821 ATCGTCTTCACCAGCCTCTTCGCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 ATCGTCTTCACCAGCCTCTTCGCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC 2400

Qy      2881 TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCATTGTGGTCATCAGTGTG 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCATTGTGGTCATCAGTGTG 2460

Qy      2941 TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCTGATG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCTGATG 2520

Qy      3001 CGGGTGCTGAAGCTGGTGCGCTTCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 CGGGTGCTGAAGCTGGTGCGCTTCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG 2580

Qy      3061 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTC 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTC 2640

Qy      3121 AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG 3180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2641 AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG 2700

Qy      3181 TTGCCAGACCGGAAGAATTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT 3240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2701 TTGCCAGACCGGAAGAATTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT 2760

Qy      3241 CTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTTGG 3300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2761 CTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTTGG 2820

Qy      3301 GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 3360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2821 GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 2880

Qy      3361 GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG 3420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2881 GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG 2940

Qy      3421 CCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG 3480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2941 CCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG 3000

Qy      3481 GTGGCTTTGGGAGAACACGCGGAACTACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT 3540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3001 GTGGCTTTGGGAGAACACGCGGAACTACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT 3060

Qy      3541 ACGGCTGCGACACCAATGTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG 3600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3061 ACGGCTGCGACACCAATGTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG 3120

Qy      3601 GGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT 3660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3121 GGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT 3180
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Qy      3661 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3181 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3240

Qy      3721 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCCAGCCTAAAGCGG 3780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3241 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCCAGCCTAAAGCGG 3300

Qy      3781 AGGAGCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3301 AGGAGCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3360

Qy      3841 GAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACAGG 3900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3361 GAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACAGG 3420

Qy      3901 GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3421 GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3480

Qy      3961 GGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 4020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3481 GGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 3540

Qy      4021 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCCTGAGGACTGATGACCCCCAACTGGATGGG 4080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3541 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCCTGAGGACTGATGACCCCCAACTGGATGGG 3600

Qy      4081 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTCAGA 4140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3601 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTCAGA 3660

Qy      4141 TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCCTGGTCGGCCTATATCTTTCCTCCT 4200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3661 TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCCTGGTCGGCCTATATCTTTCCTCCT 3720

Qy      4201 CAGTCAAGGTTTCGTCTCCTGTGTCACCGGATCATCACCCACAAGATGTTTGACCATGTG 4260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3721 CAGTCAAGGTTTCGTCTCCTGTGTCACCGGATCATCACCCACAAGATGTTTGACCATGTG 3780

Qy      4261 GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC 4320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3781 GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC 3840

Qy      4321 CCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACTACATCTTCACGGCAGTCTTT 4380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3841 CCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACTACATCTTCACGGCAGTCTTT 3900

Qy      4381 CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC 4440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3901 CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC 3960

Qy      4441 CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC 4500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC 4020

Qy      4501 CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG 4560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG 4080
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Qy      4561 CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGGTG 4620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGGTG 4140

Qy      4621 GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC 4680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC 4200

Qy      4681 TTCTTCATCATTTTTGGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT 4740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 TTCTTCATCATTTTTGGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT 4260

Qy      4741 CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA 4800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4261 CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA 4320

Qy      4801 TGGGTCCGGCACAAGTACAACTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG 4860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4321 TGGGTCCGGCACAAGTACAACTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG 4380

Qy      4861 CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG 4920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4381 CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG 4440

Qy      4921 GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC 4980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4441 GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC 4500

Qy      4981 CTCATCGTGGCCTTCTTTGTCCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCCAT 5040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4501 CTCATCGTGGCCTTCTTTGTCCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCCAT 4560

Qy      5041 AAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG 5100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4561 AAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG 4620

Qy      5101 AGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCA------------------------- 5135
             |||||||||||||||||||||| |     |  | |
Db      4621 AGGCTGGAGAAAAAGAGAAGGAATCTAATGTTGGACGATGTAATTGCTTCCGGCAGCTCA 4680

Qy      5136 --------GATGGCCGAAGCCCAGTGCAAGCCCTACTACTCTGACTACTCGAGATTCCGG 5187
                        | | |||||||||||||||||||||||||||||||||||||||||||||
Db      4681 GCCAGCGCTGCGTCAGAAGCCCAGTGCAAGCCCTACTACTCTGACTACTCGAGATTCCGG 4740

Qy      5188 CTCCTTGTCCACCACCTGTGTACCAGCCACTACCTGGACCTCTTCATCACTGGTGTCATC 5247
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4741 CTCCTTGTCCACCACCTGTGTACCAGCCACTACCTGGACCTCTTCATCACTGGTGTCATC 4800

Qy      5248 GGGCTGAACGTGGTCACTATGGCCATGGAACATTACCAGCAGCCCCAGATCCTGGACGAG 5307
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4801 GGGCTGAACGTGGTCACTATGGCCATGGAACATTACCAGCAGCCCCAGATCCTGGACGAG 4860

Qy      5308 GCTCTGAAGATCTGCAATTACATCTTTACCGTCATCTTTGTCTTTGAGTCAGTTTTCAAA 5367
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4861 GCTCTGAAGATCTGCAATTACATCTTTACCGTCATCTTTGTCTTTGAGTCAGTTTTCAAA 4920

Qy      5368 CTTGTGGCCTTTGCGTTCCGCCGTTTCTTCCAGGACAGGTGGAACCAGCTGGACCTGGCT 5427
             |||||||||||||  |||||||||||||||||||||||||||||||||||||||||||||
Db      4921 CTTGTGGCCTTTGGCTTCCGCCGTTTCTTCCAGGACAGGTGGAACCAGCTGGACCTGGCT 4980
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Qy     5428 ATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATCTGTCGCTG 5487
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4981 ATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAGATTGAGGTCAATCTGTCGCTG 5040

Qy     5488 CCCATCAACCCCACCATCATCCGTATCATGAGGGTGCTCCGCATTGCTCGAGTTCTGAAG 5547
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5041 CCCATCAACCCCACCATCATCCGTATCATGAGGGTGCTCCGCATTGCTCGAGTTCTGAAG 5100

Qy     5548 CTGTTGAAGATGGCTGTGGGCATGCGGGCACTGCTGCACACGGTGATGCAGGCCCTGCCC 5607
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5101 CTGTTGAAGATGGCTGTGGGCATGCGGGCACTGCTGCACACGGTGATGCAGGCCCTGCCC 5160

Qy     5608 CAGGTGGGGAACCTGGGACTTCTCTTCATGTTATTGTTTTTCATCTTTGCAGCTCTGGGC 5667
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5161 CAGGTGGGGAACCTGGGACTTCTCTTCATGTTATTGTTTTTCATCTTTGCAGCTCTGGGC 5220

Qy     5668 GTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCTTGTGAGGGCTTGGGTCGG 5727
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5221 GTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACACCCTTGTGAGGGCTTGGGTCGG 5280

Qy     5728 CATGCCACCTTTAGGAACTTTGGTATGGCCTTTCTGACCCTCTTCCGAGTCTCCACTGGT 5787
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5281 CATGCCACCTTTAGGAACTTTGGTATGGCCTTTCTGACCCTCTTCCGAGTCTCCACTGGT 5340

Qy     5788 GACAACTGGAATGGTATTATGAAGGACCCTTCCCGGGACTGTGACCAGGAGTCCACCTGC 5847
            ||||||||||||||||||||||||||| |   ||||||||||||||||||||||||||||
Db     5341 GACAACTGGAATGGTATTATGAAGGACACCCTCCGGGACTGTGACCAGGAGTCCACCTGC 5400

Qy     5848 TACAACACTGTCATCTCCCCTATCTACTTTGTGTCCTTCGTGCTGACGGCCCAGTTTGTG 5907
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5401 TACAACACTGTCATCTCCCCTATCTACTTTGTGTCCTTCGTGCTGACGGCCCAGTTTGTG 5460

Qy     5908 CTGGTCAACGTGGTCATAGCTGTGCTGATGAAGCACCTGGAAGAAAGCAACAAAGAGGCC 5967
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5461 CTGGTCAACGTGGTCATAGCTGTGCTGATGAAGCACCTGGAAGAAAGCAACAAAGAGGCC 5520

Qy     5968 AAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAAGACGCTCAGCCCGCAG 6027
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5521 AAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGCTGGAGATGAAGACGCTCAGCCCGCAG 5580

Qy     6028 CCCCACTCCCCGCTGGGCAGCCCCTTCCTCTGGCCCGGGGTGGAGGGTGTCAACAGTACT 6087
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5581 CCCCACTCCCCGCTGGGCAGCCCCTTCCTCTGGCCCGGGGTGGAGGGTGTCAACAGTACT 5640

Qy     6088 GACAGCCCTAAGCCTGGGGCTCCACACACCACTGCCCACATTGGAGCAGCCTCGGGCTTC 6147
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5641 GACAGCCCTAAGCCTGGGGCTCCACACACCACTGCCCACATTGGAGCAGCCTCGGGCTTC 5700

Qy     6148 TCCCTTGAGCACCCCACGATGGTACCCCACCCCGAGGAGGTGCCAGTCCCCCTAGGACCA 6207
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5701 TCCCTTGAGCACCCCACGATGGTACCCCACCCCGAGGAGGTGCCAGTCCCCCTAGGACCA 5760

Qy     6208 GACCTGCTGACTGTGAGGAAGTCTGGTGTCAGCCGGACGCACTCTCTGCCCAATGACAGC 6267
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5761 GACCTGCTGACTGTGAGGAAGTCTGGTGTCAGCCGGACGCACTCTCTGCCCAATGACAGC 5820

Qy     6268 TACATGTGCCGCAATGGGAGCACTGCTGAGAGATCCCTAGGACACAGGGGCTGGGGGCTC 6327
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5821 TACATGTGCCGCAATGGGAGCACTGCTGAGAGATCCCTAGGACACAGGGGCTGGGGGCTC 5880
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Qy     6328 CCCAAAGCCCAGTCAGGCTCCATCTTGTCCGTTCACTCCCAACCAGCAGACACCAGCTGC 6387
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5881 CCCAAAGCCCAGTCAGGCTCCATCTTGTCCGTTCACTCCCAACCAGCAGACACCAGCTGC 5940

Qy     6388 ATCCTACAGCTTCCCAAAGATGTGCACTATCTGCTCCAGCCTCATGGGGCTCCCACCTGG 6447
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     5941 ATCCTACAGCTTCCCAAAGATGTGCACTATCTGCTCCAGCCTCATGGGGCTCCCACCTGG 6000

Qy     6448 GGCGCCATCCCTAAACTACCCCCACCTGGCCGCTCCCCTCTGGCTCAGAGGCCTCTCAGG 6507
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6001 GGCGCCATCCCTAAACTACCCCCACCTGGCCGCTCCCCTCTGGCTCAGAGGCCTCTCAGG 6060

Qy     6508 CGCCAGGCAGCAATAAGGACTGACTCCCTGGATGTGCAGGGCCTGGGTAGCCGGGAAGAC 6567
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6061 CGCCAGGCAGCAATAAGGACTGACTCCCTGGATGTGCAGGGCCTGGGTAGCCGGGAAGAC 6120

Qy     6568 CTGTTGTCAGAGGTGAGTGGGCCCTCCTGCCCTCTGACCCGGTCCTCATCCTTCTGGGGC 6627
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6121 CTGTTGTCAGAGGTGAGTGGGCCCTCCTGCCCTCTGACCCGGTCCTCATCCTTCTGGGGC 6180

Qy     6628 GGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAGAGCAAAGTCTCCAAGCACATC 6687
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6181 GGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAGAGCAAAGTCTCCAAGCACATC 6240

Qy     6688 CGCCTGCCAGCCCCTTGCCCAGGCCTGGAACCCAGCTGGGCCAAGGACCCTCCAGAGACC 6747
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6241 CGCCTGCCAGCCCCTTGCCCAGGCCTGGAACCCAGCTGGGCCAAGGACCCTCCAGAGACC 6300

Qy     6748 AGAAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATTTCAGGAGACCTCCTTCCCAGC 6807
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6301 AGAAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATTTCAGGAGACCTCCTTCCCAGC 6360

Qy     6808 AGCCAGGAAGAACCCCTGTTCCCACGGGACCTGAAGAAGTGCTACAGTGTAGAGACCCAG 6867
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6361 AGCCAGGAAGAACCCCTGTTCCCACGGGACCTGAAGAAGTGCTACAGTGTAGAGACCCAG 6420

Qy     6868 AGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGATGAACAGCGGAGACACTCCATTGCTGTC 6927
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6421 AGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGATGAACAGCGGAGACACTCCATTGCTGTC 6480

Qy     6928 AGCTGTCTGGACAGCGGCTCCCAACCCCGCCTATGTCCAAGCCCCTCAAGCCTCGGGGGC 6987
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6481 AGCTGTCTGGACAGCGGCTCCCAACCCCGCCTATGTCCAAGCCCCTCAAGCCTCGGGGGC 6540

Qy     6988 CAACCTCTTGGGGGTCCTGGGAGCCGGCCTAAGAAAAAACTCAGCCCACCCAGTATCTCT 7047
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6541 CAACCTCTTGGGGGTCCTGGGAGCCGGCCTAAGAAAAAACTCAGCCCACCCAGTATCTCT 6600

Qy     7048 ATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCCCCATGCAGTCCTGGTGTCTGCCTCAGG 7107
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6601 ATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCCCCATGCAGTCCTGGTGTCTGCCTCAGG 6660

Qy     7108 AGGAGGGCGCCGGCCAGTGACTCTAAGGATCCCTCGGTCTCCAGCCCCCTTGACAGCACG 7167
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6661 AGGAGGGCGCCGGCCAGTGACTCTAAGGATCCCTCGGTCTCCAGCCCCCTTGACAGCACG 6720

Qy     7168 GCTGCCTCACCCTCCCCAAAGAAAGACACGCTGAGTCTCTCTGGTTTGTCTTCTGACCCA 7227
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     6721 GCTGCCTCACCCTCCCCAAAGAAAGACACGCTGAGTCTCTCTGGTTTGTCTTCTGACCCA 6780
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Qy       7228 ACAGACATGGACCCC 7242
              |||||||||||||||
Db       6781 ACAGACATGGACCCC 6795


RESULT 7
AAX83487
ID   AAX83487 standard; cDNA; 6816 BP.
XX
AC   AAX83487;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1c) cDNA.
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy; ds.
XX
OS   Rattus sp.
XX
PN   WO9929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E,  Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   P-PSDB; AAY14592.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 85-94; 138pp; English.
XX
CC   This sequence represents the coding region for a rat T-type voltage-gated
CC   calcium (Ca) channel alpha-1-G designated rCavT1c. Voltage gated channels
CC   are membrane bound glycosylated proteins formed of several subunits. The
CC   large alpha subunits form a pore in the membrane that is selective for a
CC   given ionic species. Each alpha subunit contains 4 domains (I, II, III
CC   and IV) and each domain contains 6 putative transmembrane helical
CC   segments (S1-S6). T-type Ca channels are activated at a lower voltage
CC   than L- or N-type channels. Characteristics of T-type channels include
CC   short current time, slow activation kinetics near threshold, fast
CC   inactivation kinetics and slow tail current. The sequences AAX83481-
CC   X83492 represent novel T-type voltage-gated Ca channel genes from humans
CC   and rats. Each of the novel Ca-channels contains a putative IVS4 region
CC   comprising the amino acid sequence AAY14598. Cells expressing the T-type
CC   voltage-gated calcium channel proteins can be used to screen for drugs
CC   which affect calcium channels. Methods are also disclosed for treating a
CC   disease or disorder associated with a deficiency in a native T-type
CC   calcium channel nucleic acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 6816 BP; 1373 A; 2058 C; 1932 G; 1453 T; 0 U; 0 Other;
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  Query Match             88.4%;  Score 6661.6;  DB 2;  Length 6816;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 6746;  Conservative    0;  Mismatches   14;  Indels   56;  Gaps    2;

Qy        483 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGACGAGGAGGAGGATGGAGCGGGCGCCGAGGAGTCGGGACAGCCCCGTAGCTTCACG 60

Qy        543 CAGCTCAACGACCTGTCCGGGGCCGGGGC--GGCAGGGGCCGGGTCGACGGAAAAGGAC 600
              |||||||||||||||||||||||||||||   |   ||| | ||||||||||||||||||
Db         61 CAGCTCAACGACCTGTCCGGGGCCGGGGGCCGGCAGGGGCCGGGGTCGACGGAAAAGGAC 120

Qy        601 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCGGGCAGCGCGGACTCCGAGGCGGAGGGGCTGCCGTACCCGGCGCTAGCCCCGGTGGTT 180

Qy        661 TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCTTCTACTTGAGCCAGGACAGCCGCCCGCGGAGCTGGTGTCTCCGCACGGTCTGTAAC 240

Qy        721 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CCGTGGTTCGAGCGAGTCAGTATGCTGGTCATTCTTCTCAACTGTGTGACTCTGGGTATG 300

Qy        781 TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCAGGCCGTGTGAGGACATTGCCTGTGACTCCCAGCGCTGCCGGATCCTGCAGGCCTTC 360

Qy        841 GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GATGACTTCATCTTTGCCTTCTTTGCTGTGGAAATGGTGGTGAAGATGGTGGCCTTGGGC 420

Qy        901 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTCATTGTC 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCTTTGGGAAGAAATGTTACCTGGGAGACACTTGGAACCGGCTTGACTTTTTCATTGTC 480

Qy        961 ATTGCAGGGATGCTGGAGTATTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATTGCAGGGATGCTGGAGTATTCGCTGGACCTGCAGAACGTCAGCTTCTCCGCAGTCAGG 540

Qy       1021 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCCAGCATGCGCATTCTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACAGTCCGTGTGCTGCGACCGCTCAGGGCCATTAACCGGGTGCCCAGCATGCGCATTCTC 600

Qy       1081 GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCACATTACTGCTGGACACCTTGCCTATGCTGGGCAACGTCCTGCTGCTCTGTTTCTTC 660

Qy       1141 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTCTTTTTCATCTTTGGCATCGTGGGCGTCCAGCTGTGGGCAGGACTGCTTCGCAACCGG 720

Qy       1201 TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGCTTCCTCCCCGAGAACTTCAGCCTCCCCCTGAGCGTGGACCTGGAGCCTTATTACCAG 780

Qy       1261 ACAGAGAATGAGGACGAGAGCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 ACAGAGAATGAGGACGAGAGCCCCTTCATCTGCTCTCAGCCTCGGGAGAATGGCATGAGA 840
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Qy        1321 TCCTGCAGGAGTGTGCCCACACTGCGTGGGGAAGGCGGTGGTGGCCCACCCTGCAGTCTG 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TCCTGCAGGAGTGTGCCCACACTGCGTGGGGAAGGCGGTGGTGGCCCACCCTGCAGTCTG 900

Qy        1381 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT 1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GACTATGAGACCTATAACAGTTCCAGCAACACCACCTGTGTCAACTGGAACCAGTACTAT 960

Qy        1441 ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 ACCAACTGCTCTGCGGGCGAGCACAACCCCTTCAAAGGCGCCATCAACTTTGACAACATT 1020

Qy        1501 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 GGCTATGCCTGGATCGCCATCTTCCAGGTCATCACACTGGAGGGCTGGGTCGACATCATG 1080

Qy        1561 TACTTCGTAATGGACGCTCACTCCTTCTACAACTTCATCTACTTCATTCTTCTCATCATC 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 TACTTCGTAATGGACGCTCACTCCTTCTACAACTTCATCTACTTCATTCTTCTCATCATC 1140

Qy        1621 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1680
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 GTGGGCTCCTTCTTCATGATCAACCTGTGCCTGGTGGTGATTGCCACGCAGTTCTCCGAG 1200

Qy        1681 ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGTACGATTCCTGTCCAATGCT 1740
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 ACCAAACAGCGGGAGAGTCAGCTGATGCGGGAGCAGCGTGTACGATTCCTGTCCAATGCT 1260

Qy        1741 AGCACCCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1800
               || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 AGTACCCTGGCAAGCTTCTCTGAGCCAGGCAGCTGCTATGAGGAGCTACTCAAGTACCTG 1320

Qy        1801 GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCGTG 1860
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 GTGTACATCCTCCGAAAAGCAGCCCGAAGGCTGGCCCAGGTCTCTAGGGCTATAGGCGTG 1380

Qy        1861 CGGGCTGGGCTGCTCAGCAGCCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCCAGTGGC 1920
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CGGGCTGGGCTGCTCAGCAGCCCAGTGGCCCGTAGTGGGCAGGAGCCCCAGCCCAGTGGC 1440

Qy        1921 AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC 1980
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 AGCTGCACTCGCTCACACCGTCGTCTGTCTGTCCACCACCTGGTCCACCACCATCACCAC 1500

Qy        1981 CACCATCACCACTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCCAGAG 2040
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 CACCATCACCACTACCACCTGGGTAATGGGACGCTCAGAGTTCCCCGGGCCAGCCCAGAG 1560

Qy        2041 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCCTCTACACCC 2100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 ATCCAGGACAGGGATGCCAATGGGTCTCGCCGGCTCATGCTACCACCACCCTCTACACCC 1620

Qy        2101 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 2160
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1621 ACTCCCTCTGGGGGCCCTCCGAGGGGTGCGGAGTCTGTACACAGCTTCTACCATGCTGAC 1680

Qy        2161 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCCTCCCAGATGCCCATCGGAGGCATCT 2220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1681 TGCCACTTGGAGCCAGTCCGTTGCCAGGCACCCCCTCCCAGATGCCCATCGGAGGCATCT 1740
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Qy      2221 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAG 2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 GGTAGGACTGTGGGTAGTGGGAAGGTGTACCCCACTGTGCATACCAGCCCTCCACCAGAG 1800

Qy      2281 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCTCACC 2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1801 ATACTGAAGGATAAAGCACTAGTGGAGGTGGCCCCCAGCCCTGGGCCCCCCACCCTCACC 1860

Qy      2341 AGCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1861 AGCTTCAACATCCCACCTGGGCCCTTCAGCTCCATGCACAAGCTCCTGGAGACACAGAGT 1920

Qy      2401 ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGA 2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1921 ACGGGAGCCTGCCATAGCTCCTGCAAAATCTCCAGCCCTTGCTCCAAGGCAGACAGTGGA 1980

Qy      2461 GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGTCC 2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1981 GCCTGCGGGCCGGACAGTTGTCCCTACTGTGCCCGGACAGGAGCAGGAGAGCCAGAGTCC 2040

Qy      2521 GCTGACCATGTCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT 2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2041 GCTGACCATGTCATGCCTGACTCAGACAGCGAGGCTGTGTATGAGTTCACACAGGACGCT 2100

Qy      2581 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGGAGCCTGGGCCCAGAT 2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2101 CAGCACAGTGACCTCCGGGATCCCCACAGCCGGCGGCGACAGCGGAGCCTGGGCCCAGAT 2160

Qy      2641 GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC 2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2161 GCAGAGCCTAGTTCTGTGCTGGCTTTCTGGAGGCTGATCTGTGACACATTCCGGAAGATC 2220

Qy      2701 GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC 2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2221 GTAGATAGCAAATACTTTGGCCGGGGAATCATGATCGCCATCCTGGTCAATACACTCAGC 2280

Qy      2761 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2281 ATGGGCATCGAGTACCACGAGCAGCCCGAGGAGCTCACCAACGCCCTGGAAATCAGCAAC 2340

Qy      2821 ATCGTCTTCACCAGCCTCTTCGCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC 2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2341 ATCGTCTTCACCAGCCTCTTCGCCTTGGAGATGCTGCTGAAACTGCTTGTCTACGGTCCC 2400

Qy      2881 TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCATTGTGGTCATCAGTGTG 2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2401 TTTGGCTACATTAAGAATCCCTACAACATCTTTGATGGTGTCATTGTGGTCATCAGTGTG 2460

Qy      2941 TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCTGATG 3000
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2461 TGGGAGATTGTGGGCCAGCAGGGAGGTGGCCTGTCGGTGCTGCGGACCTTCCGCCTGATG 2520

Qy      3001 CGGGTGCTGAAGCTGGTGCGCTTCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG 3060
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2521 CGGGTGCTGAAGCTGGTGCGCTTCCTGCCGGCCCTGCAGCGCCAGCTCGTGGTGCTCATG 2580

Qy      3061 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTC 3120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2581 AAGACCATGGACAACGTGGCCACCTTCTGCATGCTCCTCATGCTGTTCATCTTCATCTTC 2640
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Qy   3121 AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG 3180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2641 AGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACACG 2700

Qy   3181 TTGCCAGACCGGAAGAATTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT 3240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2701 TTGCCAGACCGGAAGAATTTCGACTCCCTGCTCTGGGCCATCGTCACTGTCTTTCAGATT 2760

Qy   3241 CTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTTGG 3300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2761 CTGACTCAGGAAGACTGGAATAAAGTCCTCTACAACGGCATGGCCTCCACATCGTCTTGG 2820

Qy   3301 GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 3360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2821 GCTGCTCTTTACTTCATCGCCCTCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTG 2880

Qy   3361 GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG 3420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2881 GTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAGAG 2940

Qy   3421 CCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG 3480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2941 CCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCCTG 3000

Qy   3481 GTGGCTTTGGGAGAACACGCGGAACTACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT 3540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3001 GTGGCTTTGGGAGAACACGCGGAACTACGAAAGAGCCTTTTGCCACCCCTCATCATCCAT 3060

Qy   3541 ACGGCTGCGACACCAATGTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG 3600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3061 ACGGCTGCGACACCAATGTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCACTG 3120

Qy   3601 GGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT 3660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3121 GGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACCAT 3180

Qy   3661 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3181 GAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAAGC 3240

Qy   3721 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCCAGCCTAAAGCGG 3780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3241 AGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCCAGCCTAAAGCGG 3300

Qy   3781 AGGAGCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3301 AGGAGCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGGAT 3360

Qy   3841 GAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACAGG 3900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 GAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACAGG 3420

Qy   3901 GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 GGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGCCG 3480

Qy   3961 GGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 4020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 GGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATGGC 3540
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Qy    4021 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCCTGAGGACTGATGACCCCCAACTGGATGGG 4080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3541 AAGTCGGCTTCAGGGCGTTTGGCCCGCACCCTGAGGACTGATGACCCCCAACTGGATGGG 3600

Qy    4081 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGTCAGA 4140
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    3601 GATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCAGACAAGCCTGGTCAGA 3660

Qy    4141 TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCCTGGTCGGCCTATATCTTTCCTCCT 4200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3661 TCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCCTGGTCGGCCTATATCTTTCCTCCT 3720

Qy    4201 CAGTCAAGGTTTCGTCTCCTGTGTCACCGGATCATCACCCACAAGATGTTTGACCATGTG 4260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3721 CAGTCAAGGTTTCGTCTCCTGTGTCACCGGATCATCACCCACAAGATGTTTGACCATGTG 3780

Qy    4261 GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC 4320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3781 GTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTGAC 3840

Qy    4321 CCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACTACATCTTCACGGCAGTCTTT 4380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3841 CCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACTACATCTTCACGGCAGTCTTT 3900

Qy    4381 CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC 4440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3901 CTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCTAC 3960

Qy    4441 CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC 4500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3961 CTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACATC 4020

Qy    4501 CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG 4560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4021 CTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGCGG 4080

Qy    4561 CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGGTG 4620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4081 CTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGGTG 4140

Qy    4621 GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC 4680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4141 GTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTGCC 4200

Qy    4681 TTCTTCATCATTTTTGGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT 4740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4201 TTCTTCATCATTTTTGGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGTGT 4260

Qy    4741 CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA 4800
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4261 CAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACCGA 4320

Qy    4801 TGGGTCCGGCACAAGTACAACTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG 4860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4321 TGGGTCCGGCACAAGTACAACTTTGACAACCTGGGCCAGGCTCTGATGTCCCTGTTTGTG 4380

Qy    4861 CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG 4920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4381 CTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTGTG 4440
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Qy        4921 GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC 4980
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4441 GATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCCTC 4500

Qy        4981 CTCATCGTGGCCTTCTTTGTCCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCCAT 5040
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4501 CTCATCGTGGCCTTCTTTGTCCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCCAT 4560

Qy        5041 AAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG 5100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4561 AAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTACGG 4620

Qy        5101 AGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCC------------------ 5142
               ||||||||||||||||||||||||||||||||||||||||||
Db        4621 AGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCCGATCTAATGTTGGACGAT 4680

Qy        5143 ------------------------------------GAAGCCCAGTGCAAGCCCTACTAC 5166
                                                   ||||||||||||||||||||||||
Db        4681 GTAATTGCTTCCGGCAGCTCAGCCAGCGCTGCGTCAGAAGCCCAGTGCAAGCCCTACTAC 4740

Qy        5167 TCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTACCTGGAC 5226
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4741 TCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACTACCTGGAC 4800

Qy        5227 CTCTTCATCACTGGTGTCATCGGGCTGAACGTGGTCACTATGGCCATGGAACATTACCAG 5286
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4801 CTCTTCATCACTGGTGTCATCGGGCTGAACGTGGTCACTATGGCCATGGAACATTACCAG 4860

Qy        5287 CAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCATCTTT 5346
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4861 CAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCGTCATCTTT 4920

Qy        5347 GTCTTTGAGTCAGTTTTCAAACTTGTGGCCTTTGCGTTCCGCCGTTTCTTCCAGGACAGG 5406
               ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        4921 GTCTTTGAGTCAGTTTTCAAACTTGTGGCCTTTGGCTTCCGCCGTTTCTTCCAGGACAGG 4980

Qy        5407 TGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAG 5466
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        4981 TGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACACTGGAGGAG 5040

Qy        5467 ATTGAGGTCAATCTGTCGCTGCCCATCAACCCCACCATCATCCGTATCATGAGGGTGCTC 5526
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5041 ATTGAGGTCAATCTGTCGCTGCCCATCAACCCCACCATCATCCGTATCATGAGGGTGCTC 5100

Qy        5527 CGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTGCTGCAC 5586
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5101 CGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCACTGCTGCAC 5160

Qy        5587 ACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTATTGTTT 5646
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5161 ACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGTTATTGTTT 5220

Qy        5647 TTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACAC 5706
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5221 TTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATGAGACACAC 5280

Qy        5707 CCTTGTGAGGGCTTGGGTCGGCATGCCACCTTTAGGAACTTTGGTATGGCCTTTCTGACC 5766
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        5281 CCTTGTGAGGGCTTGGGTCGGCATGCCACCTTTAGGAACTTTGGTATGGCCTTTCTGACC 5340
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Qy   5767 CTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACCCTTCCCGGGAC 5826
          |||||||||||||||||||||||||||||||||||||||||||||||| |   |||||||
Db   5341 CTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACACCCTCCGGGAC 5400

Qy   5827 TGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTGTGTCCTTC 5886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5401 TGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTGTGTCCTTC 5460

Qy   5887 GTGCTGACGGCCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAGCACCTG 5946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5461 GTGCTGACGGCCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGAAGCACCTG 5520

Qy   5947 GAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGCTGGAG 6006
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5521 GAAGAAAGCAACAAAGAGGCCAAGGAGGAGGCCGAGCTCGAGGCCGAGCTGGAGCTGGAG 5580

Qy   6007 ATGAAGACGCTCAGCCCGCAGCCCCACTCCCCGCTGGGCAGCCCCTTCCTCTGGCCCGGG 6066
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5581 ATGAAGACGCTCAGCCCGCAGCCCCACTCCCCGCTGGGCAGCCCCTTCCTCTGGCCCGGG 5640

Qy   6067 GTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACTGCCCAC 6126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5641 GTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCACTGCCCAC 5700

Qy   6127 ATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCCACGATGGTACCCCACCCCGAGGAG 6186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5701 ATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCCACGATGGTACCCCACCCCGAGGAG 5760

Qy   6187 GTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTCAGCCGGACG 6246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5761 GTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTCAGCCGGACG 5820

Qy   6247 CACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGATCCCTA 6306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5821 CACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGAGATCCCTA 5880

Qy   6307 GGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCGTTCACTCC 6366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5881 GGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCGTTCACTCC 5940

Qy   6367 CAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATCTGCTCCAG 6426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   5941 CAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATCTGCTCCAG 6000

Qy   6427 CCTCATGGGGCTCCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCCGCTCCCCT 6486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6001 CCTCATGGGGCTCCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCCGCTCCCCT 6060

Qy   6487 CTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGATGTGCAG 6546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6061 CTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGGATGTGCAG 6120

Qy   6547 GGCCTGGGTAGCCGGGAAGACCTGTTGTCAGAGGTGAGTGGGCCCTCCTGCCCTCTGACC 6606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6121 GGCCTGGGTAGCCGGGAAGACCTGTTGTCAGAGGTGAGTGGGCCCTCCTGCCCTCTGACC 6180

Qy   6607 CGGTCCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAG 6666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   6181 CGGTCCTCATCCTTCTGGGGCGGGTCGAGCATCCAGGTGCAGCAGCGTTCCGGCATCCAG 6240
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Qy       6667 AGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCTTGCCCAGGCCTGGAACCCAGCTGG 6726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6241 AGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCTTGCCCAGGCCTGGAACCCAGCTGG 6300

Qy       6727 GCCAAGGACCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATT 6786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6301 GCCAAGGACCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGAGCTGGATT 6360

Qy       6787 TCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCCTGTTCCCACGGGACCTGAAGAAG 6846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Db       6361 TCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCCTGTTCCCACGGGACCTGAAGAAC 6420

Qy       6847 TGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGATGAACAG 6906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6421 TGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAGATGAACAG 6480

Qy       6907 CGGAGACACTCCATTGCTGTCAGCTGTCTGGACAGCGGCTCCCAACCCCGCCTATGTCCA 6966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6481 CGGAGACACTCCATTGCTGTCAGCTGTCTGGACAGCGGCTCCCAACCCCGCCTATGTCCA 6540

Qy       6967 AGCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCCTGGGAGCCGGCCTAAGAAAAAA 7026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6541 AGCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCCTGGGAGCCGGCCTAAGAAAAAA 6600

Qy       7027 CTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCCCCATGC 7086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6601 CTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGCCCCCATGC 6660

Qy       7087 AGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATCCCTCGGTC 7146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6661 AGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATCCCTCGGTC 6720

Qy       7147 TCCAGCCCCCTTGACAGCACGGCTGCCTCACCCTCCCCAAAGAAAGACACGCTGAGTCTC 7206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6721 TCCAGCCCCCTTGACAGCACGGCTGCCTCACCCTCCCCAAAGAAAGACACGCTGAGTCTC 6780

Qy       7207 TCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC 7242
              ||||||||||||||||||||||||||||||||||||
Db       6781 TCTGGTTTGTCTTCTGACCCAACAGACATGGACCCC 6816
```

Proteins

Run on: February 9, 2007, 00:38:40 ; Search time 287 Seconds
(without alignments)
3899.322 Million cell updates/sec

Title: US-09-346-794-24
Perfect score: 12028
Sequence: 1 MLPHRVPRCVRTPPLRGSAR..........KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*
11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12028	100.0	2287	4	AAB66475	Aab66475 Rat alpha
2	11657	96.9	2254	2	AAY14590	Aay14590 Rat T-typ
3	11626	96.7	2272	2	AAY14592	Aay14592 Rat T-typ
4	11610.5	96.5	2265	2	AAY14591	Aay14591 Rat T-typ
5	11606.5	96.5	2247	2	AAY14593	Aay14593 Rat T-typ
6	11542.5	96.0	2428	3	AAY70720	Aay70720 Rat pancr
7	10857	90.3	2250	2	AAY14586	Aay14586 Human T-t
8	10838	90.1	2268	9	AEC95659	Aec95659 Calcium c
9	10838	90.1	2268	9	AEE17869	Aee17869 Human T-t
10	10838	90.1	2268	10	AEI99662	Aei99662 Human CCA
11	10833	90.1	2268	2	AAY14588	Aay14588 Human T-t
12	10820.5	90.0	2273	4	AAE01019	Aae01019 Human T-t
13	10810.5	89.9	2261	2	AAY14587	Aay14587 Human T-t
14	10806.5	89.8	2243	2	AAY14589	Aay14589 Human T-t
15	10806.5	89.8	2243	7	ADJ68819	Adj68819 Human hea
16	10732.5	89.2	2377	8	ADQ89064	Adq89064 Human uro
17	10732.5	89.2	2377	10	AEI99755	Aei99755 Human CCA
18	10533	87.6	2266	4	AAB66481	Aab66481 Human alp
19	7274	60.5	1513	9	AEC95660	Aec95660 Calcium c
20	7274	60.5	1513	10	AEI99663	Aei99663 Human CCA
21	7252.5	60.3	1504	10	AEI99760	Aei99760 Human CCA
22	6246	51.9	2359	9	AEC05419	Aec05419 Rat T-typ
23	6243	51.9	2359	9	AEC05417	Aec05417 Rat T-typ
24	6243	51.9	2359	9	AEC05415	Aec05415 Rat T-typ
25	6226.5	51.8	2359	4	AAB66476	Aab66476 Rat alpha
26	6222	51.7	2353	2	AAY06299	Aay06299 Human act
27	6222	51.7	2353	6	ABP72254	Abp72254 Human T-t
28	6222	51.7	2353	7	ADJ69322	Adj69322 Human hea
29	6222	51.7	2353	10	AEI99763	Aei99763 Human CCA

30	6221	51.7	2353	2	AAY06298	Aay06298 Human act
31	6217	51.7	2347	9	AEC95642	Aec95642 Calcium c
32	6217	51.7	2347	10	AEI99645	Aei99645 Human CCA
33	6195.5	51.5	2353	5	ABG30840	Abg30840 Human vol
34	5872	48.8	1207	4	AAU00474	Aau00474 Human T-t
35	5872	48.8	1207	10	AEK52293	Aek52293 Human T-t
36	5835	48.5	2044	2	AAY14594	Aay14594 Human T-t
37	5827	48.4	2038	2	AAY14595	Aay14595 Human T-t
38	5718.5	47.5	2034	2	AAY06300	Aay06300 Human act
39	5409	45.0	2175	5	AAU10535	Aau10535 Human T-t
40	5409	45.0	2175	6	ABU08511	Abu08511 Human T-t
41	5409	45.0	2175	8	ADH69265	Adh69265 Human TCC
42	5405.5	44.9	2188	5	AAU10536	Aau10536 Human T-t
43	5405.5	44.9	2188	6	ABU08512	Abu08512 Human T-t
44	5405.5	44.9	2188	8	ADH69267	Adh69267 Human TCC
45	5361.5	44.6	1981	9	ADZ58492	Adz58492 Human alp

ALIGNMENTS

```
RESULT 2
AAY14590
ID   AAY14590 standard; protein; 2254 AA.
XX
AC   AAY14590;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1a).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Rattus sp.
XX
PN   WO9929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E,  Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83485.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 67-76; 138pp; English.
XX
CC   This sequence represents a rat T-type voltage-gated calcium (Ca) channel
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CC   alpha-1-G designated rCavT1a. Voltage gated channels are membrane bound
CC   glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2254 AA;

  Query Match             96.9%;  Score 11657;  DB 2;  Length 2254;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2219;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
              |  | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 GRQGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 89

Qy        122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy        182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy        242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269

Qy        302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy        362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy        422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy        482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN 509

Qy        542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569

Qy        602 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 661
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    570 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 629

Qy    662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689

Qy    722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    690 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

Qy    782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 809

Qy    842 IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    810 IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 869

Qy    902 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    870 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 929

Qy    962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 989

Qy   1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1049

Qy   1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1050 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1109

Qy   1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1110 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1169

Qy   1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE 1261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1170 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE 1229

Qy   1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289

Qy   1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1290 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1349

Qy   1382 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1350 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1409

Qy   1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1410 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1469

Qy   1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1561
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1470 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1529

Qy        1562 EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1621
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1530 EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1589

Qy        1622 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLA 1681
               |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db        1590 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFGFRRFFQDRWNQLDLA 1649

Qy        1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1741
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1650 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1709

Qy        1742 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1801
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1710 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1769

Qy        1802 DNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1861
               |||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db        1770 DNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1829

Qy        1862 KEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1830 KEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1889

Qy        1922 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1981
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1890 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1949

Qy        1982 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2041
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1950 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2009

Qy        2042 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2101
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2010 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2069

Qy        2102 RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQ 2161
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2070 RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQ 2129

Qy        2162 SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS 2221
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2130 SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS 2189

Qy        2222 IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP 2281
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2190 IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP 2249

Qy        2282 TDMDP 2286
               |||||
Db        2250 TDMDP 2254


RESULT 3
AAY14592
ID   AAY14592 standard; protein; 2272 AA.
XX
```

```
AC   AAY14592;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1c).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Rattus sp.
XX
PN   WO9929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E,  Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83487.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 85-94; 138pp; English.
XX
CC   This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC   alpha-1-G designated rCavT1c. Voltage gated channels are membrane bound
CC   glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2272 AA;

  Query Match             96.7%;  Score 11626;  DB 2;  Length 2272;
  Best Local Similarity   98.8%;  Pred. No. 0;
  Matches 2217;  Conservative    0;  Mismatches    8;  Indels   18;  Gaps    1;

Qy         62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
              |  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 GRQGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 89

Qy        122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db           90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy          182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy          242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269

Qy          302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          270 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy          362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy          422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy          482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN 541
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          450 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN 509

Qy          542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569

Qy          602 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 661
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          570 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 629

Qy          662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689

Qy          722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          690 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

Qy          782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 809

Qy          842 IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          810 IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 869

Qy          902 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          870 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 929

Qy          962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 989

Qy         1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1049

Qy     1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1050 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1109

Qy     1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1110 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1169

Qy     1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE 1261
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     1170 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERRQAWVRSRLPACCRE 1229

Qy     1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289

Qy     1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1290 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1349

Qy     1382 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1350 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1409

Qy     1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1501
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1410 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1469

Qy     1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1561
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1470 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1529

Qy     1562 EARRREEKRLRRLEKKRRSKEKQMA------------------EAQCKPYYSDYSRFRLL 1603
            |||||||||||||||||||||||||                  |||||||||||||||||
Db     1530 EARRREEKRLRRLEKKRRSKEKQMADLMLDDVIASGSSASAASEAQCKPYYSDYSRFRLL 1589

Qy     1604 VHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLV 1663
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1590 VHHLCTSHYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLV 1649

Qy     1664 AFAFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLL 1723
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1650 AFGFRRFFQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLL 1709

Qy     1724 KMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHA 1783
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1710 KMAVGMRALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHA 1769

Qy     1784 TFRNFGMAFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLV 1843
            |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db     1770 TFRNFGMAFLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLV 1829

Qy     1844 NVVIAVLMKHLEESNKEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDS 1903
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1830 NVVIAVLMKHLEESNKEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDS 1889

Qy     1904 PKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYM 1963
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1890 PKPGAPHTTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYM 1949

Qy       1964 CRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGA 2023
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1950 CRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGA 2009

Qy       2024 IPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGS 2083
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2010 IPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGS 2069

Qy       2084 SIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQ 2143
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2070 SIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQ 2129

Qy       2144 EEPLFPRDLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQP 2203
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       2130 EEPLFPRDLKNCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQP 2189

Qy       2204 LGGPGSRPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAA 2263
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2190 LGGPGSRPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAA 2249

Qy       2264 SPSPKKDTLSLSGLSSDPTDMDP 2286
              |||||||||||||||||||||||
Db       2250 SPSPKKDTLSLSGLSSDPTDMDP 2272
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RESULT 4
AAY14591
ID   AAY14591 standard; protein; 2265 AA.
XX
AC   AAY14591;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1b).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Rattus sp.
XX
PN   WO9929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E,  Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83486.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 76-85; 138pp; English.
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XX
CC   This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC   alpha-1-G designated rCavT1b. Voltage gated channels are membrane bound
CC   glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2265 AA;

  Query Match             96.5%;  Score 11610.5;  DB 2;  Length 2265;
  Best Local Similarity   99.0%;  Pred. No. 0;
  Matches 2213;  Conservative    1;  Mismatches   11;  Indels   11;  Gaps    1;

Qy         62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
              |  | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 GRQGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 89

Qy        122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy        182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy        242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269

Qy        302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy        362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy        422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy        482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN 509

Qy        542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569
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Qy    602 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 661
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    570 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 629

Qy    662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689

Qy    722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    690 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

Qy    782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 809

Qy    842 IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    810 IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 869

Qy    902 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    870 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 929

Qy    962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 989

Qy   1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1049

Qy   1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1050 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1109

Qy   1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1110 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1169

Qy   1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE 1261
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1170 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE 1229

Qy   1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289

Qy   1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1290 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1349

Qy   1382 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1350 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1409

Qy   1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1501
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1410 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1469
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Qy          1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1561
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1470 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1529

Qy          1562 EARRREEKRLRRLEKKRR-----------SKEKQMAEAQCKPYYSDYSRFRLLVHHLCTS 1610
                 ||||||||||||||||||           |     :||||||||||||||||||||||||
Db          1530 EARRREEKRLRRLEKKRRNLMLDDVIASGSSASAASEAQCKPYYSDYSRFRLLVHHLCTS 1589

Qy          1611 HYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRF 1670
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          1590 HYLDLFITGVIGLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFGFRRF 1649

Qy          1671 FQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR 1730
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1650 FQDRWNQLDLAIVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMR 1709

Qy          1731 ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM 1790
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1710 ALLHTVMQALPQVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGM 1769

Qy          1791 AFLTLFRVSTGDNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVL 1850
                 ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Db          1770 AFLTLFRVSTGDNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVL 1829

Qy          1851 MKHLEESNKEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPH 1910
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1830 MKHLEESNKEAKEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPH 1889

Qy          1911 TTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA 1970
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1890 TTAHIGAASGFSLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTA 1949

Qy          1971 ERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPP 2030
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1950 ERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPP 2009

Qy          2031 GRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQR 2090
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2010 GRSPLAQRPLRRQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQR 2069

Qy          2091 SGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPR 2150
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2070 SGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPR 2129

Qy          2151 DLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSR 2210
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2130 DLKKCYSVETQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSR 2189

Qy          2211 PKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKD 2270
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2190 PKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKD 2249

Qy          2271 TLSLSGLSSDPTDMDP 2286
                 ||||||||||||||||
Db          2250 TLSLSGLSSDPTDMDP 2265
```

RESULT 5
AAY14593

```
ID   AAY14593 standard; protein; 2247 AA.
XX
AC   AAY14593;
XX
DT   07-DEC-1999  (first entry)
XX
DE   Rat T-type voltage-gated Ca channel alpha-1-G (rCavT1d).
XX
KW   Human; T-type voltage-gated calcium channel; membrane; pore; ion;
KW   activation; current; rat; screen; drug; cardiomyopathy; epilepsy.
XX
OS   Rattus sp.
XX
PN   WO9929847-A1.
XX
PD   17-JUN-1999.
XX
PF   30-OCT-1998;   98WO-US023161.
XX
PR   05-DEC-1997;   97US-00985809.
XX
PA   (LOYO ) UNIV LOYOLA CHICAGO.
XX
PI   Perez-Reyes E,  Cribbs LL;
XX
DR   WPI; 1999-394972/33.
DR   N-PSDB; AAX83488.
XX
PT   New T-type voltage-gated calcium channels.
XX
PS   Disclosure; Page 94-103; 138pp; English.
XX
CC   This sequence represents a rat T-type voltage-gated calcium (Ca) channel
CC   alpha-1-G designated rCavT1d. Voltage gated channels are membrane bound
CC   glycosylated proteins formed of several subunits. The large alpha
CC   subunits form a pore in the membrane that is selective for a given ionic
CC   species. Each alpha subunit contains 4 domains (I, II, III and IV) and
CC   each domain contains 6 putative transmembrane helical segments (S1-S6). T
CC   -type Ca channels are activated at a lower voltage than L- or N-type
CC   channels. Characteristics of T-type channels include short current time,
CC   slow activation kinetics near threshold, fast inactivation kinetics and
CC   slow tail current. The sequences AAX83481-X83492 represent novel T-type
CC   voltage-gated Ca channel genes from humans and rats. Each of the novel Ca
CC   -channels contains a putative IVS4 region comprising the amino acid
CC   sequence AAY14598. Cells expressing the T-type voltage-gated calcium
CC   channel proteins can be used to screen for drugs which affect calcium
CC   channels. Methods are also disclosed for treating a disease or disorder
CC   associated with a deficiency in a native T-type calcium channel nucleic
CC   acid, e.g. to treat cardiomyopathy, epilepsy, etc
XX
SQ   Sequence 2247 AA;

  Query Match             96.5%;  Score 11606.5;  DB 2;  Length 2247;
                           Best Local Similarity   99.4%;  Pred. No. 0;
  Matches 2211;  Conservative    1;  Mismatches    6;  Indels    7;  Gaps    1;

Qy         62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
              |  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 GRQGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 89
```

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Qy     122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy     182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy     242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269

Qy     302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     270 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy     362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy     422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy     482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN 541
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     450 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN 509

Qy     542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569

Qy     602 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 661
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     570 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 629

Qy     662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689

Qy     722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     690 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

Qy     782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 809

Qy     842 IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     810 IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 869

Qy     902 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     870 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 929

Qy     962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 989
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Qy    1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1049

Qy    1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1050 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1109

Qy    1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1110 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1169

Qy    1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE 1261
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1170 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE 1229

Qy    1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289

Qy    1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1290 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1349

Qy    1382 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1350 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1409

Qy    1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1410 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1469

Qy    1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1470 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1529

Qy    1562 EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1621
           ||||||||||||||||||       :||||||||||||||||||||||||||||||||||
Db    1530 EARRREEKRLRRLEKKRR-------KAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1582

Qy    1622 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLA 1681
           |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db    1583 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFGFRRFFQDRWNQLDLA 1642

Qy    1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1741
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1643 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1702

Qy    1742 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1801
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1703 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1762

Qy    1802 DNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1861
           |||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db    1763 DNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1822

Qy    1862 KEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1823 KEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1882
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Qy    1922 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1981
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1883 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1942

Qy    1982 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2041
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1943 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2002

Qy    2042 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2101
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2003 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2062

Qy    2102 RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQ 2161
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2063 RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQ 2122

Qy    2162 SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS 2221
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2123 SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS 2182

Qy    2222 IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP 2281
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2183 IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP 2242

Qy    2282 TDMDP 2286
           |||||
Db    2243 TDMDP 2247
```

Appendix B

Database search of nucleic acid and polypeptide sequence with the greatest identity to SEQ ID NO :23 and SEQ ID NO:24 are provided below. A comparison of the sequences disclosed by Perez-Reyes, W. (Nature, Vol. 391, pages 900,1998) that have greatest identity with SEQ ID NO :23 and SEQ ID NO:24 are provided in detail.

```
Run on:         February  9, 2007, 10:42:19 ; Search time 44042 Seconds
                                             (without alignments)
                                             11833.410 Million cell updates/sec

Title:          US-09-346-794-23
Perfect score:  7540
Sequence:       1 ccgtctctggcgcggagcgg..........acgtttgtgcagaatctcta 7540

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters:      15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       GenEmbl:*
                1:  gb_env:*
                2:  gb_pat:*
                3:  gb_ph:*
                4:  gb_pl:*
                5:  gb_pr:*
                6:  gb_ro:*
                7:  gb_sts:*
                8:  gb_sy:*
                9:  gb_un:*
                10:  gb_vi:*
                11:  gb_ov:*
                12:  gb_htg:*
                13:  gb_in:*
                14:  gb_om:*
                15:  gb_ba:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7540	100.0	7540	2	AX068898	AX068898 Sequence
2	7510.4	99.6	7542	6	RNCAA1G	AF027984 Rattus no
3	6956.4	92.3	7286	6	AF125161	AF125161 Rattus no
4	6955.4	92.2	7285	2	BD224079	BD224079 T-type ca
5	6910.4	91.6	6942	6	AF290212	AF290212 Rattus no
6	6816.6	90.4	7129	2	BD224078	BD224078 T-type ca
7	6607.2	87.6	7527	6	BC057399	BC057399 Mus muscu
8	6492.2	86.1	7281	6	DQ317412	DQ317412 Mus muscu
9	6401	84.9	7625	6	MMU012569	AJ012569 Mus muscu
10	5810.6	77.1	7741	2	BD407048	BD407048 DNA ENCOD
11	5810.6	77.1	7741	2	AR201015	AR201015 Sequence
12	5758.6	76.4	7512	5	BC110995	BC110995 Homo sapi
13	5737.2	76.1	7349	5	AF190860	AF190860 Homo sapi
14	5714.8	75.8	7274	5	AF126966	AF126966 Homo sapi
15	5664.4	75.1	7253	5	AF126965	AF126965 Homo sapi
16	5507.8	73.0	6768	5	DQ494455	DQ494455 Homo sapi
17	5457.4	72.4	6747	5	DQ494450	DQ494450 Homo sapi
18	5444	72.2	6801	5	DQ494453	DQ494453 Homo sapi
19	5436.6	72.1	6786	5	AF227747	AF227747 Homo sapi
20	5428.8	72.0	6837	5	DQ494468	DQ494468 Homo sapi
21	5421.4	71.9	6822	5	AF227744	AF227744 Homo sapi
22	5419.8	71.9	6822	2	BD407047	BD407047 DNA ENCOD
23	5419.8	71.9	6822	2	AR201014	AR201014 Sequence
24	5399	71.6	7825	2	DD222996	DD222996 Genes for
25	5378.4	71.3	6816	5	DQ494459	DQ494459 Homo sapi
26	5371	71.2	6801	5	AF227751	AF227751 Homo sapi
27	5365	71.2	6870	5	DQ494464	DQ494464 Homo sapi
28	5364.8	71.2	6891	5	DQ494471	DQ494471 Homo sapi
29	5364.8	71.2	6912	5	DQ494456	DQ494456 Homo sapi
30	5357.6	71.1	6855	5	AF227749	AF227749 Homo sapi
31	5357.4	71.1	6897	5	AF227746	AF227746 Homo sapi
32	5351	71.0	6698	5	DQ494449	DQ494449 Homo sapi
33	5337.6	70.8	6752	5	DQ494452	DQ494452 Homo sapi
34	5326.4	70.6	6795	5	DQ494457	DQ494457 Homo sapi
35	5322.4	70.6	6788	5	DQ494466	DQ494466 Homo sapi
36	5313	70.5	6849	5	DQ494461	DQ494461 Homo sapi
37	5303	70.3	6921	5	AF227748	AF227748 Homo sapi
38	5295.6	70.2	6731	5	DQ494451	DQ494451 Homo sapi
39	5285.8	70.1	6981	5	DQ494469	DQ494469 Homo sapi
40	5278.4	70.0	6966	5	AF227745	AF227745 Homo sapi
41	5275.2	70.0	6762	5	DQ494477	DQ494477 Homo sapi
42	5272	69.9	6767	5	DQ494458	DQ494458 Homo sapi
43	5263.2	69.8	6756	5	DQ494478	DQ494478 Homo sapi
44	5258.6	69.7	6821	5	DQ494462	DQ494462 Homo sapi
45	5238	69.5	6699	5	DQ494472	DQ494472 Homo sapi

ALIGNMENTS

```
RESULT 2
RNCAA1G
LOCUS       RNCAA1G                 7542 bp    mRNA    linear   ROD 24-OCT-1998
DEFINITION  Rattus norvegicus low voltage-activated, T-type calcium channel
            alpha subunit (CACNA1G) mRNA, complete cds.
ACCESSION   AF027984
VERSION     AF027984.1  GI:3786350
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
REFERENCE   1  (bases 1 to 7542)
  AUTHORS   Perez-Reyes,E., Cribbs,L.L., Daud,A., Lacerda,A.E., Barclay,J.,
            Williamson,M.P., Fox,M., Rees,M. and Lee,J.H.
  TITLE     Molecular characterization of a neuronal low-voltage-activated
            T-type calcium channel
  JOURNAL   Nature 391 (6670), 896-900 (1998)
   PUBMED   9495342
REFERENCE   2  (bases 1 to 7542)
  AUTHORS   Cribbs,L.L., Yang,J., Daud,A., Lee,J.-H. and Perez-Reyes,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-OCT-1997) Physiology, Loyola University Medical
            Center, 2160 South First Avenue, Maywood, IL 60153, USA
REFERENCE   3  (bases 1 to 7542)
  AUTHORS   Cribbs,L.L., Yang,J., Daud,A., Lee,J.-H. and Perez-Reyes,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-OCT-1998) Physiology, Loyola University Medical
            Center, 2160 South First Avenue, Maywood, IL 60153, USA
  REMARK    Sequence update by submitter
COMMENT     On Oct 24, 1998 this sequence version replaced gi:2921748.
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ORIGIN

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Qy   3119 TCAGCATCCTGGGCATGCATCTCTTTGGTTGCAAGTTCGCATCTGAACGGGATGGGGACA 3178
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Qy   3359 TGGTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAG 3418
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3361 TGGTGGCCATTCTTGTGGAAGGATTCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTCAG 3420

Qy   3419 AGCCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCC 3478
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3421 AGCCTGATTTCTTTTCGCCCAGTGTGGATGGTGATGGGGACAGAAAGAAGCGCTTGGCCC 3480

Qy   3479 TGGTGGCTTTGGGAGAACACGCGGAACTACGAAAGAGCCTTTTGCCACCCCTCATCATCC 3538
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3481 TGGTGGCTTTGGGAGAACACGCGGAACTACGAAAGAGCCTTTTGCCACCCCTCATCATCC 3540

Qy   3539 ATACGGCTGCGACACCAATGTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCAC 3598
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3541 ATACGGCTGCGACACCAATGTCACACCCCAAGAGCTCCAGCACAGGTGTGGGGGAAGCAC 3600

Qy   3599 TGGGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACC 3658
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3601 TGGGCTCTGGCTCTCGACGTACCAGTAGCAGTGGGTCCGCTGAGCCTGGAGCTGCCCACC 3660

Qy   3659 ATGAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAA 3718
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3661 ATGAGATGAAATGTCCGCCAAGTGCCCGCAGCTCCCCGCACAGTCCCTGGAGTGCGGCAA 3720

Qy   3719 GCAGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCCAGCCTAAAGC 3778
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3721 GCAGCTGGACCAGCAGGCGCTCCAGCAGGAACAGCCTGGGCCGGGCCCCCAGCCTAAAGC 3780

Qy   3779 GGAGGAGCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGG 3838
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3781 GGAGGAGCCCGAGCGGGGAGCGGAGGTCCCTGCTGTCTGGAGAGGGCCAGGAGAGTCAGG 3840

Qy   3839 ATGAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACA 3898
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3841 ATGAGGAGGAAAGTTCAGAAGAGGACCGGGCCAGCCCAGCAGGCAGTGACCATCGCCACA 3900
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Qy       3899 GGGGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGC 3958
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Db       3901 GGGGTTCCTTGGAACGTGAGGCCAAGAGTTCCTTTGACCTGCCTGACACTCTGCAGGTGC 3960

Qy       3959 CGGGGCTGCACCGCACAGCCAGCGGCCGGAGCTCTGCCTCTGAGCACCAAGACTGTAATG 4018
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Qy       4019 GCAAGTCGGCTTCAGGGCGTTTGGCCCGCACCCTGAGGACTGATGACCCCCAACTGGATG 4078
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Db       4021 GCAAGTCGGCTTCAGGGCGTTTGGCCCGCACCCTGAGGACTGATGACCCCCAACTGGATG 4080

Qy       4079 GGGATGATGACAATGATGAGGGAAATCTGAGCAAAGGGGAACGCATACAAGCCTGGGTCA 4138
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Qy       4139 GATCCCGGCTTCCTGCCTGTTGCCGAGAGCGAGATTCCTGGTCGGCCTATATCTTTCCTC 4198
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Qy       4199 CTCAGTCAAGGTTTCGTCTCCTGTGTCACCGGATCATCACCCACAAGATGTTTGACCATG 4258
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Qy       4259 TGGTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTG 4318
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Db       4261 TGGTCCTCGTCATCATCTTCCTCAACTGTATCACCATCGCTATGGAGCGCCCCAAAATTG 4320

Qy       4319 ACCCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACTACATCTTCACGGCAGTCT 4378
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Db       4321 ACCCCCACAGCGCTGAGCGCATCTTCCTGACCCTCTCCAACTACATCTTCACGGCAGTCT 4380

Qy       4379 TTCTAGCTGAAATGACAGTGAAGGTGGTGGCACTGGGCTGGTGCTTTGGGGAGCAGGCCT 4438
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Qy       4439 ACCTGCGCAGCAGCTGGAATGTGCTGGACGGCTTGCTGGTGCTCATCTCCGTCATCGACA 4498
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Qy       4499 TCCTGGTCTCCATGGTCTCCGACAGCGGCACCAAGATCCTTGGCATGCTGAGGGTGCTGC 4558
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Qy       4559 GGCTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGG 4618
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Db       4561 GGCTGCTGCGGACCCTGCGTCCACTCAGGGTCATCAGCCGGGCCCAGGGACTGAAGCTGG 4620

Qy       4619 TGGTAGAGACTCTGATGTCATCCCTCAAACCCATTGGCAACATTGTGGTCATTTGCTGTG 4678
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Qy       4679 CCTTCTTCATCATTTTTGGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGT 4738
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Db       4681 CCTTCTTCATCATTTTTGGAATTCTCGGGGTGCAGCTCTTCAAAGGGAAGTTCTTCGTGT 4740

Qy       4739 GTCAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACC 4798
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Db         4741 GTCAGGGTGAGGACACCAGGAACATCACTAACAAATCCGACTGCGCTGAGGCCAGCTACC 4800

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Qy         4859 TGCTGGCCTCCAAGGATGGTTGGGTTGACATCATGTATGATGGGCTGGATGCTGTGGGTG 4918
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Qy         4919 TGGATCAGCAGCCCATCATGAACCACAACCCCTGGATGCTGCTATACTTCATCTCCTTCC 4978
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Qy         4979 TCCTCATCGTGGCCTTCTTTGTCCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCC 5038
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Db         4981 TCCTCATCGTGGCCTTCTTTGTCCTGAACATGTTTGTGGGCGTGGTGGTGGAGAACTTCC 5040

Qy         5039 ATAAGTGCAGACAGCACCAGGAGGAGGAGGAGGCGAGGCGGCGTGAGGAGAAGCGACTAC 5098
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Qy         5099 GGAGGCTGGAGAAAAAGAGAAGGAGTAAGGAGAAGCAGATGGCCGAAGCCCAGTGCAAGC 5158
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Qy         5159 CCTACTACTCTGACTACTCGAGATTCCGGCTCCTTGTCCACCACCTGTGTACCAGCCACT 5218
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Qy         5219 ACCTGGACCTCTTCATCACTGGTGTCATCGGGCTGAACGTGGTCACTATGGCCATGGAAC 5278
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Qy         5279 ATTACCAGCAGCCCCAGATCCTGGACGAGGCTCTGAAGATCTGCAATTACATCTTTACCG 5338
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Qy         5339 TCATCTTTGTCTTTGAGTCAGTTTTCAAACTTGTGGCCTTTGCGTTCCGCCGTTTCTTCC 5398
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Qy         5399 AGGACAGGTGGAACCAGCTGGACCTGGCTATTGTGCTTCTGTCCATCATGGGCATCACAC 5458
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Qy         5459 TGGAGGAGATTGAGGTCAATCTGTCGCTGCCCATCAACCCCACCATCATCCGTATCATGA 5518
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Qy         5519 GGGTGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCAC 5578
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Db         5521 GGGTGCTCCGCATTGCTCGAGTTCTGAAGCTGTTGAAGATGGCTGTGGGCATGCGGGCAC 5580

Qy         5579 TGCTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGT 5638
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Db         5581 TGCTGCACACGGTGATGCAGGCCCTGCCCCAGGTGGGGAACCTGGGACTTCTCTTCATGT 5640

Qy         5639 TATTGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATG 5698
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Db    5641 TATTGTTTTTCATCTTTGCAGCTCTGGGCGTGGAGCTCTTTGGAGACCTGGAGTGTGATG 5700

Qy    5699 AGACACACCCTTGTGAGGGCTTGGGTCGGCATGCCACCTTTAGGAACTTTGGTATGGCCT 5758
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Db    5701 AGACACACCCTTGTGAGGGCTTGGGTCGGCATGCCACCTTTAGGAACTTTGGTATGGCCT 5760

Qy    5759 TTCTGACCCTCTTCCGAGTCTCCACTGGTGACAACTGGAATGGTATTATGAAGGACCCTT 5818
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Qy    5819 CCCGGGACTGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTG 5878
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Db    5821 TCCGGGACTGTGACCAGGAGTCCACCTGCTACAACACTGTCATCTCCCCTATCTACTTTG 5880

Qy    5879 TGTCCTTCGTGCTGACGGCCCAGTTTGTGCTGGTCAACGTGGTCATAGCTGTGCTGATGA 5938
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Qy    5999 AGCTGGAGATGAAGACGCTCAGCCCGCAGCCCCACTCCCCGCTGGGCAGCCCCTTCCTCT 6058
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Qy    6059 GGCCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCA 6118
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Db    6061 GGCCCGGGGTGGAGGGTGTCAACAGTACTGACAGCCCTAAGCCTGGGGCTCCACACACCA 6120

Qy    6119 CTGCCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCCACGATGGTACCCCACC 6178
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Db    6121 CTGCCCACATTGGAGCAGCCTCGGGCTTCTCCCTTGAGCACCCCACGATGGTACCCCACC 6180

Qy    6179 CCGAGGAGGTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTCA 6238
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Db    6181 CCGAGGAGGTGCCAGTCCCCCTAGGACCAGACCTGCTGACTGTGAGGAAGTCTGGTGTCA 6240

Qy    6239 GCCGGACGCACTCTCTGCCCAATGACAGCTACATGTGCCGCAATGGGAGCACTGCTGAGA 6298
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Qy    6299 GATCCCTAGGACACAGGGGCTGGGGGCTCCCCAAAGCCCAGTCAGGCTCCATCTTGTCCG 6358
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Qy    6359 TTCACTCCCAACCAGCAGACACCAGCTGCATCCTACAGCTTCCCAAAGATGTGCACTATC 6418
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Qy    6419 TGCTCCAGCCTCATGGGGCTCCCACCTGGGGCGCCATCCCTAAACTACCCCCACCTGGCC 6478
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Qy    6479 GCTCCCCTCTGGCTCAGAGGCCTCTCAGGCGCCAGGCAGCAATAAGGACTGACTCCCTGG 6538
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Qy    6539 ATGTGCAGGGCCTGGGTAGCCGGGAAGACCTGTTGTCAGAGGTGAGTGGGCCCTCCTGCC 6598
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Db        6541 ATGTGCAGGGCCTGGGTAGCCGGGAAGACCTGTTGTCAGAGGTGAGTGGGCCCTCCTGCC 6600

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Db        6661 GCATCCAGAGCAAAGTCTCCAAGCACATCCGCCTGCCAGCCCCTTGCCCAGGCCTGGAAC 6720

Qy        6719 CCAGCTGGGCCAAGGACCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGA 6778
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Db        6721 CCAGCTGGGCCAAGGACCCTCCAGAGACCAGAAGCAGCTTAGAGCTGGACACGGAGCTGA 6780

Qy        6779 GCTGGATTTCAGGAGACCTCCTTCCCAGCAGCCAGGAAGAACCCCTGTTCCCACGGGACC 6838
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Qy        6839 TGAAGAAGTGCTACAGTGTAGAGACCCAGAGCTGCAGGCGCAGGCCTGGGTTCTGGCTAG 6898
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Qy        6959 TATGTCCAAGCCCCTCAAGCCTCGGGGGCCAACCTCTTGGGGGTCCTGGGAGCCGGCCTA 7018
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Qy        7019 AGAAAAAACTCAGCCCACCCAGTATCTCTATAGACCCCCCGGAGAGCCAGGGCTCTCGGC 7078
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Qy        7079 CCCCATGCAGTCCTGGTGTCTGCCTCAGGAGGAGGGCGCCGGCCAGTGACTCTAAGGATC 7138
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Qy        7139 CCTCGGTCTCCAGCCCCCTTGACAGCACGGCTGCCTCACCCTCCCCAAAGAAAGACACGC 7198
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Qy        7439 GCCCCTGCCTCCGGGAAGAAGGAAAAGGAGAAGCCCAGTGTGGCCAAGGCTCCCGACACC 7498
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Db          7441 GCCCCTGCCTCCGGGAAGAAGGAAAAGGAGAAGCCCAGTGTGGCCAAGGCTCCCGACACC 7500

Qy          7499 AGGAGCTGTTGGGAGAAGCAATACGTTTGTGCAGAATCTCTA 7540
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Db          7501 AGGAGCTGTTGGGAGAAGCAATACGTTTGTGCAGAATCTCTA 7542
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Run on:          February  9, 2007, 00:44:55 ; Search time 67 Seconds
                                               (without alignments)
                                               3284.295 Million cell updates/sec

Title:           US-09-346-794-24
Perfect score:   12028
Sequence:        1 MLPHRVPRCVRTPPLRGSAR..........KKDTLSLSGLSSDPTDMDPZ 2287

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:      283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        PIR_80:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                  SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	11657	96.9	2254	2	T09053	low voltage-activa
2	3553	29.5	1657	2	T15838	hypothetical prote
3	1720.5	14.3	1810	2	T31092	probable voltage-g
4	1676	13.9	2339	2	A42566	omega-conotoxin-se
5	1665.5	13.8	2259	2	S29236	calcium channel pr
6	1653.5	13.7	2272	2	C54972	voltage-dependent
7	1652.5	13.7	1891	2	T43262	calcium channel al
8	1652.5	13.7	2178	2	S29237	calcium channel pr
9	1650.5	13.7	2288	2	S41080	calcium channel al
10	1642	13.7	2223	2	A47447	calcium channel pr
11	1640.5	13.6	2237	2	T45115	N-type calcium cha
12	1638	13.6	2251	2	B54972	voltage-dependent
13	1637.5	13.6	2270	2	A54972	voltage-dependent
14	1636	13.6	1993	2	T30902	sodium channel SCA
15	1632.5	13.6	2222	2	A37490	voltage-dependent
16	1632.5	13.6	2336	2	A45386	omega-conotoxin-se
17	1631	13.6	2181	2	A38198	calcium channel al
18	1628	13.5	1873	2	A30063	dihydropyridine re
19	1622	13.5	2161	2	JH0564	calcium channel al
20	1619.5	13.5	1911	2	T43048	calcium channel al
21	1616	13.4	1852	2	A37860	calcium channel pr
22	1614.5	13.4	1977	2	S54771	sodium channel alp
23	1613	13.4	2203	2	T42742	voltage-dependent
24	1610	13.4	2143	2	JH0427	voltage-dependent
25	1603	13.3	1610	2	A46227	voltage-dependent
26	1595.5	13.3	1783	2	T37258	probable voltage-d
27	1595	13.3	2166	2	S11339	calcium channel pr
28	1592.5	13.2	2139	2	A44467	voltage-dependent
29	1587.5	13.2	1646	2	JH0422	voltage-dependent
30	1587.5	13.2	1873	2	A55645	calcium channel, v
31	1585.5	13.2	2016	2	A38195	sodium channel pro
32	1580	13.1	1917	2	C88728	protein C48A7.1 [i
33	1577.5	13.1	1559	2	T30535	calcium channel al
34	1574	13.1	2171	2	S05054	calcium channel al
35	1573	13.1	2108	2	S72458	sodium channel pro
36	1567.5	13.0	1687	2	S41742	calcium channel al
37	1565	13.0	1957	2	S68453	sodium channel pro
38	1557.5	12.9	2220	2	A45290	calcium channel pr
39	1556	12.9	2019	2	A33996	sodium channel pro
40	1551.5	12.9	1840	1	CHRTM1	sodium channel pro
41	1549	12.9	1976	2	I56555	sodium channel pro
42	1546.5	12.9	1983	2	A60054	sodium channel pro
43	1546	12.9	2262	2	T30890	calcium channel al
44	1544.5	12.8	1951	2	S00320	sodium channel pro
45	1544.5	12.8	2005	2	A46269	sodium channel alp

ALIGNMENTS

RESULT 1
T09053
low voltage-activated, T-type calcium channel alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

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C;Accession: T09053
R;Perez-Reyes, E.; Cribbs, L.L.; Daud, A.; Lacerda, A.; Barclay, J.; Williamson, M.;
Fox, M.; Rees, M.; Lee, J.H.
Nature 391, 896, 1998
A;Title: Molecular characterization of a neuronal low voltage-activated, T-type,
calcium channel.
A;Reference number: Z16538; MUID:98154730; PMID:9495342
A;Accession: T09053
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2254
A;Cross-references: UNIPROT:O54898; UNIPARC:UPI00000009B4; EMBL:AF027984;
NID:g3786350; PIDN:AAC67372.1; PID:g3786351
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Map position: 17
A;Note: CACNA1G
C;Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C;Keywords: calcium channel; voltage-gated ion channel

  Query Match             96.9%;  Score 11657;  DB 2;  Length 2254;
  Best Local Similarity   99.7%;  Pred. No. 0;
  Matches 2219;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         62 GAAGAGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 121
              |  | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 GRQGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPWFERVSML 89

Qy        122 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         90 VILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLG 149

Qy        182 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        150 DTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTVRVLRPLRAINRVPSMRILVTLLLDTLP 209

Qy        242 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        210 MLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVDLEPYYQTENEDESPF 269

Qy        302 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 ICSQPRENGMRSCRSVPTLRGEGGGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHN 329

Qy        362 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        330 PFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFILLIIVGSFFMINL 389

Qy        422 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 CLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAAR 449

Qy        482 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        450 RLAQVSRAIGVRAGLLSSPVARSGQEPQPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGN 509

Qy        542 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        510 GTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGAESVHSFYHADCHLEPVRCQ 569
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Qy     602 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 661
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Db     570 APPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFNIPPGPF 629

Qy     662 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 721
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     630 SSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSCPYCARTGAGEPESADHVMPDSD 689

Qy     722 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 781
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     690 SEAVYEFTQDAQHSDLRDPHSRRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRG 749

Qy     782 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 841
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     750 IMIAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYN 809

Qy     842 IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 901
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     810 IFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPALQRQLVVLMKTMDNVATF 869

Qy     902 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 961
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     870 CMLLMLFIFIFSILGMHLFGCKFASERDGDTLPDRKNFDSLLWAIVTVFQILTQEDWNKV 929

Qy     962 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 1021
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     930 LYNGMASTSSWAALYFIALMTFGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVD 989

Qy    1022 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1081
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     990 GDGDRKKRLALVALGEHAELRKSLLPPLIIHTAATPMSHPKSSSTGVGEALGSGSRRTSS 1049

Qy    1082 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1050 SGSAEPGAAHHEMKCPPSARSSPHSPWSAASSWTSRRSSRNSLGRAPSLKRRSPSGERRS 1109

Qy    1142 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1201
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1110 LLSGEGQESQDEEESSEEDRASPAGSDHRHRGSLEREAKSSFDLPDTLQVPGLHRTASGR 1169

Qy    1202 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE 1261
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Db    1170 SSASEHQDCNGKSASGRLARTLRTDDPQLDGDDDNDEGNLSKGERIQAWVRSRLPACCRE 1229

Qy    1262 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1230 RDSWSAYIFPPQSRFRLLCHRIITHKMFDHVVLVIIFLNCITIAMERPKIDPHSAERIFL 1289

Qy    1322 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1381
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Db    1290 TLSNYIFTAVFLAEMTVKVVALGWCFGEQAYLRSSWNVLDGLLVLISVIDILVSMVSDSG 1349

Qy    1382 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1350 TKILGMLRVLRLLRTLRPLRVISRAQGLKLVVETLMSSLKPIGNIVVICCAFFIIFGILG 1409

Qy    1442 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1410 VQLFKGKFFVCQGEDTRNITNKSDCAEASYRWVRHKYNFDNLGQALMSLFVLASKDGWVD 1469
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Qy      1502 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1561
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Db      1470 IMYDGLDAVGVDQQPIMNHNPWMLLYFISFLLIVAFFVLNMFVGVVVENFHKCRQHQEEE 1529

Qy      1562 EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1621
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Db      1530 EARRREEKRLRRLEKKRRSKEKQMAEAQCKPYYSDYSRFRLLVHHLCTSHYLDLFITGVI 1589

Qy      1622 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFAFRRFFQDRWNQLDLA 1681
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db      1590 GLNVVTMAMEHYQQPQILDEALKICNYIFTVIFVFESVFKLVAFGFRRFFQDRWNQLDLA 1649

Qy      1682 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1741
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Db      1650 IVLLSIMGITLEEIEVNLSLPINPTIIRIMRVLRIARVLKLLKMAVGMRALLHTVMQALP 1709

Qy      1742 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1801
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1710 QVGNLGLLFMLLFFIFAALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLTLFRVSTG 1769

Qy      1802 DNWNGIMKDPSRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1861
             |||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Db      1770 DNWNGIMKDTLRDCDQESTCYNTVISPIYFVSFVLTAQFVLVNVVIAVLMKHLEESNKEA 1829

Qy      1862 KEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1921
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1830 KEEAELEAELELEMKTLSPQPHSPLGSPFLWPGVEGVNSTDSPKPGAPHTTAHIGAASGF 1889

Qy      1922 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1981
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1890 SLEHPTMVPHPEEVPVPLGPDLLTVRKSGVSRTHSLPNDSYMCRNGSTAERSLGHRGWGL 1949

Qy      1982 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1950 PKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLR 2009

Qy      2042 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2101
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Db      2010 RQAAIRTDSLDVQGLGSREDLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHI 2069

Qy      2102 RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQ 2161
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Db      2070 RLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSSQEEPLFPRDLKKCYSVETQ 2129

Qy      2162 SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS 2221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2130 SCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSIS 2189

Qy      2222 IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP 2281
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2190 IDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLDSTAASPSPKKDTLSLSGLSSDP 2249

Qy      2282 TDMDP 2286
             |||||
Db      2250 TDMDP 2254
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